

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:54:37 ; Search time 63.95 Seconds
(without alignments)
4069.212 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	ID	DB	
1	4797	100.0	921	5	ABP74104		Abp74104 Human TRI
2	4797	100.0	921	5	ABB83246		Abb83246 Human tra
3	4797	100.0	921	5	ABB81913		Abb81913 Human ion
4	4790	99.9	921	5	ABB81915		Abb81915 Human ion
5	4786.5	99.8	922	5	ABB81916		Abb81916 Human ion
6	4784	99.7	927	5	AAM47745		Aam47745 Human nat
7	4779.5	99.6	922	5	ABB81917		Abb81917 Human ion
8	4686	97.7	927	5	ABB83247		Abb83247 Human tra
9	4671	97.4	925	6	ABU12042		Abu12042 Human NOV

10	4644	96.8	895	6	ABU12043	Abu12043	Human	NOV
11	4505.5	93.9	928	6	ABU12041	Abu12041	Human	NOV
12	3425.5	71.4	970	5	AAE18291	Aae18291	Bovine	NC
13	3373.5	70.3	921	7	AAO27170	Aao27170	Human	465
14	3373.5	70.3	952	3	AAB41497	Aab41497	Human	ORF
15	3093	64.5	595	6	ABR40134	Abr40134	Human	690
16	3093	64.5	620	5	ABB81914	Abb81914	Human	ion
17	2143.5	44.7	609	4	AAM13701	Aam13701	Peptide	#
18	2143.5	44.7	609	4	ABB32633	Abb32633	Peptide	#
19	2143.5	44.7	609	4	AAM26102	Aam26102	Peptide	#
20	2143.5	44.7	609	4	ABB18131	Abb18131	Protein	#
21	2143.5	44.7	609	4	AAM53461	Aam53461	Human	bra
22	2143.5	44.7	609	4	ABG47486	Abg47486	Human	liv
23	2143.5	44.7	609	5	ABG35474	Abg35474	Human	pep
24	2130.5	44.4	950	4	ABB61721	Abb61721	Drosophil	
25	1607	33.5	394	4	ABG26781	Abg26781	Novel	hum
26	1607	33.5	394	6	ABO00862	Abo00862	Polypepti	
27	599	12.5	120	4	AAO05893	Aao05893	Human	pol
28	579	12.1	539	3	AAY58044	Aay58044	Arabidops	
29	424	8.8	91	4	AAM14216	Aam14216	Peptide	#
30	424	8.8	91	4	ABB33163	Abb33163	Peptide	#
31	424	8.8	91	4	AAM26626	Aam26626	Peptide	#
32	424	8.8	91	4	ABB27991	Abb27991	Human	pep
33	424	8.8	91	4	ABB18628	Abb18628	Protein	#
34	424	8.8	91	4	AAM66347	Aam66347	Human	bon
35	424	8.8	91	4	AAM53959	Aam53959	Human	bra
36	424	8.8	91	4	ABG48013	Abg48013	Human	liv
37	424	8.8	91	4	AAM01948	Aam01948	Peptide	#
38	424	8.8	91	5	ABG35995	Abg35995	Human	pep
39	349	7.3	123	4	AAM23946	Aam23946	Rat	EST e
40	258.5	5.4	644	7	ADE31661	Ade31661	Human	692
41	251.5	5.2	106	6	ABR40136	Abr40136	69039	pro
42	244.5	5.1	630	5	ABP69673	Abp69673	Human	pol
43	239.5	5.0	618	4	AAM78712	Aam78712	Human	pro
44	239.5	5.0	661	5	ABB84485	Abb84485	Human	NCK
45	239.5	5.0	661	6	AAO29752	Aao29752	Human	577

ALIGNMENTS

RESULT 1

ABP74104

ID ABP74104 standard; protein; 921 AA.

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AC ABP74104;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human TRICH SEQ ID NO 9.

XX

KW Human; TRICH; transporter and ion channel; transport disorder;
KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW neurological disorder; Alzheimer's disease; Huntington's disease;
KW immunological disorder; AIDS; asthma; cell proliferative disorder;
KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;

KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
 KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; virucide; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200246415-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046963.
 XX
 PR 08-DEC-2000; 2000US-0254303P.
 PR 15-DEC-2000; 2000US-0256190P.
 PR 21-DEC-2000; 2000US-0257504P.
 PR 12-JAN-2001; 2001US-0261546P.
 PR 19-JAN-2001; 2001US-0262832P.
 PR 26-JAN-2001; 2001US-0264377P.
 PR 02-FEB-2001; 2001US-0266019P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
 PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
 PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
 PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
 PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
 XX
 DR WPI; 2002-519667/55.
 DR N-PSDB; ABZ33735.
 XX
 PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
 PT prevention or treatment of transport, neurological, muscle, immunological
 PT and cell proliferative disorders.
 XX
 PS Claim 64; SEQ ID NO 9; 146pp + Sequence Listing; English.
 XX
 CC The invention relates to human transporter and ion channel polypeptide
 CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
 CC ABP74127), a naturally occurring polypeptide comprising a sequence having
 CC at least sequence 90 % identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I) and for preparing
 CC a polyclonal or monoclonal antibody by hybridoma technology.
 CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
 CC screening a compound altering gene expression. (I) and (II) are useful in
 CC a diagnostic tests for a condition or a disease associated with the
 CC expression of TRICH in a biological sample, especially disorders selected
 CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
 CC Parkinson's disease, cardiac disorders, neurological disorders such as
 CC Alzheimer's disease, Huntington's disease, muscle disorders,
 CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
 CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
 CC cancer. (II) is useful for creating knock-in humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for

CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX

SQ Sequence 921 AA;

Query Match 100.0%; Score 4797; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Db	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL	660
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL	660
Qy	661	EVIIIESEYFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS	720

Db	661	EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS	720
Qy	721	CFDYVMHFLTTFWVKVLFACVPPTTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK	780
Db	721	CFDYVMHFLTTFWVKVLFACVPPTTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK	780
Qy	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY	840
Db	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY	840
Qy	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV	900
Db	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV	900
Qy	901	SLWLLYILFATLEAYCYIKGF	921
Db	901	SLWLLYILFATLEAYCYIKGF	921

RESULT 2

ABB83246

ID ABB83246 standard; protein; 921 AA.

XX

AC ABB83246;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR N-PSDB; ABN83428, ABN83429.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
 PT for identifying modulators useful for treating a disease or condition
 PT mediated by human transporter protein.

XX

PS Claim 1; Fig 2; 200pp; English.

CC The present sequence is a human transporter protein, which is related to
CC the sodium/calcium exchanger subfamily. Experimental data indicates
CC expression of the transporter gene in humans in brain, heart, kidney,
CC lung, spleen, testis, leukocyte and foetal brain. The gene of the
CC transporter was mapped to chromosome 14 by ePCR

SQ Sequence 921 AA;

Query Match 100.0%; Score 4797; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKRIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKRIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEEAKRIAEMGKPVLGHPKL	660
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEEAKRIAEMGKPVLGHPKL	660

Qy 661 EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 661 EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720

Qy 721 CFDYVMHFLTTFWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLK 780
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 721 CFDYVMHFLTTFWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLK 780

Qy 781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840

Qy 841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGEELGGPRGCKLATTWLFV 900
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGEELGGPRGCKLATTWLFV 900

Qy 901 SLWLLYILFATLEAYCYIKGF 921
 ||||||||||||||||
 Db 901 SLWLLYILFATLEAYCYIKGF 921

RESULT 3

ABB81913

ID ABB81913 standard; protein; 921 AA.

XX

AC ABB81913;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

DR

N-PSDB; ABQ78861.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.

XX

PS Claim 2; Page 37-39; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a NHIEP of the invention

XX

SQ Sequence 921 AA;

Query Match 100.0%; Score 4797; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL 660
 |||
 Db 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL 660

Qy 661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
 |||
 Db 661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720

Qy 721 CFDYVMHFLTTFWKVLFACVPPTHEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
 |||
 Db 721 CFDYVMHFLTTFWKVLFACVPPTHEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780

Qy 781 DSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
 |||
 Db 781 DSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840

Qy 841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
 |||
 Db 841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900

Qy 901 SLWLLYILFATLEAYCYIKGF 921
 |||
 Db 901 SLWLLYILFATLEAYCYIKGF 921

RESULT 4

ABB81915

ID ABB81915 standard; protein; 921 AA.

XX

AC ABB81915;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Asp/Gly mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 630

FT /note= "Wild-type Asp substituted by Gly"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX
DR WPI; 2002-599791/64.
XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX
PS Disclosure; Page; 42pp; English.
XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)

XX
SQ Sequence 921 AA;

Query Match 99.9%; Score 4790; DB 5; Length 921;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE		120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE		120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI		180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI		180
Qy	181	IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF		240
Db	181	IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF		240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN		300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN		300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR		360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR		360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF		480

Db	421		KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF	480
Qy	481		FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481		FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541		VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541		VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Qy	601		KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHEHPKL	660
Db	601		KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHEHPKL	660
Qy	661		EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS	720
Db	661		EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS	720
Qy	721		CFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK	780
Db	721		CFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK	780
Qy	781		DSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY	840
Db	781		DSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY	840
Qy	841		WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV	900
Db	841		WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV	900
Qy	901		SLWLLYILFATLEAYCYIKGF	921
Db	901		SLWLLYILFATLEAYCYIKGF	921

RESULT 5

ABB81916

ID ABB81916 standard; protein; 922 AA.

XX

AC ABB81916;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Ala mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 704. .705

FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"

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PT

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CC

Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE	TEGDHPKGIEMDGKMMNSHFLDGN	300	
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDL	QLVEMANYYALSHQOKSRAFYRIQATR	360	
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDL	QLVEMANYYALSHQOKSRAFYRIQATR	360	
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDF	ISKVFFDPCSYQCLENCGAVLLTVVR	420	
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDF	ISKVFFDPCSYQCLENCGAVLLTVVR	420	
Qy	421	KGGDSKMTMYVDYKTEDGSANAGADYEFTEGT	VVLKPGETQKEFSVGIIIDDDIFEDEHF	480	
Db	421	KGGDSKMTMYVDYKTEDGSANAGADYEFTEGT	VVLKPGETQKEFSVGIIIDDDIFEDEHF	480	
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVL	ASPCVATVTILDDDHAGIFTFECDTIH	540	
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVL	ASPCVATVTILDDDHAGIFTFECDTIH	540	
Qy	541	VSESIGVMEVKVLR	TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET	600	
Db	541	VSESIGVMEVKVLR	TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET	600	
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVT	DRKLTMEEEEAKRIAEMGKPVLGHPKL	660	
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVT	DRKLTMEEEEAKRIAEMGKPVLGHPKL	660	
Qy	661	EVIIIEESYEFKTTVDKLIKKTNLALVVGTH	SWRDQFMEAITVS-AAGDEDEDESGEERLP	719	
Db	661	EVIIIEESYEFKTTVDKLIKKTNLALVVGTH	SWRDQFMEAITVSAAAGDEDEDESGEERLP	720	
Qy	720	SCFDYVMHFLT	TVFWKVL	FACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGL	779
Db	721	SCFDYVMHFLT	TVFWKVL	FACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGL	780
Qy	780	KDSVTAVVFVAFGTSVPD	TFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA	839	
Db	781	KDSVTAVVFVAFGTSVPD	TFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA	840	
Qy	840	YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISV	LLYRRRPHLGELGGPRGCKLATTWLF	899	
Db	841	YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISV	LLYRRRPHLGELGGPRGCKLATTWLF	900	
Qy	900	VSLWLLYILFATLEAYCYIKGF		921	
Db	901	VSLWLLYILFATLEAYCYIKGF		922	

RESULT 6

AAM47745

ID AAM47745 standard; protein; 927 AA.

XX

AC AAM47745;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human sodium(+)-calcium(2+) exchanger form 3 protein, HNCX3.

XX

Db	181	IIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPVL	654
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISGVRFFKDVTDRKLTMEEEEAKRIAEMGKPVL	660
Qy	655	GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG	714
Db	661	GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG	720
Qy	715	EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG	774
Db	721	EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG	780
Qy	775	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW	834
Db	781	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW	840
Qy	835	SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLA	894
Db	841	SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLA	900
Qy	895	TTWLFVSLWLLYILFATLEAYCYIKGF	921
Db	901	TTWLFVSLWLLYILFATLEAYCYIKGF	927

RESULT 7

ABB81917

ID ABB81917 standard; protein; 922 AA.

XX

AC ABB81917;

XX
 DT 09-OCT-2002 .(first entry)
 XX
 DE Human ion exchanger protein #1 Asp/Gly+Ala mutant.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 630
 FT /note= "Wild-type Asp substituted by Gly"
 FT Misc-difference 704. .705
 FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
 XX
 SQ Sequence 922 AA;

Query Match 99.6%; Score 4779.5; DB 5; Length 922;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 920; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy	1	MAWLRQLQPLTSAFLHFGVLTVFLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRQLQPLTSAFLHFGVLTVFLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDQVEMANYALSHQOKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDQVEMANYALSHQOKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL	660
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL	660
Qy	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVS-AAGDEDEDESGEERLP	719
Db	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAAGDEDEDESGEERLP	720
Qy	720	SCFDYVMHFLT VFWKVL FACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGL	779
Db	721	SCFDYVMHFLT VFWKVL FACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGL	780
Qy	780	KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAI	839
Db	781	KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAI	840
Qy	840	YWALQGQEFHVSAGTLAFSVTLFTIFAFVCSVLLYRRRPHLGGELEGGRGCKLATTWLF	899

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGE LGGPRGCKLATTWLF 900
Qy      900 VSLWLLYILFATLEAYCYIKGF 921
          ||||||||||||||||||
Db      901 VSLWLLYILFATLEAYCYIKGF 922

```

RESULT 8

ABB83247

ID ABB83247 standard; protein; 927 AA.

XX

AC ABB83247;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein-related protein, used in a homology alignment.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Unidentified.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
 PT for identifying modulators useful for treating a disease or condition
 PT mediated by human transporter protein.

XX

PS Disclosure; Fig 2; 200pp; English.

XX

CC The present invention relates to a human transporter protein, which is
 CC related to the sodium/calcium exchanger subfamily (ABB83246).

CC Experimental data indicates expression of the transporter gene in humans
 CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal

CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR.

CC The present protein was used in a sequence alignment with the transporter
 CC protein to illustrate the invention

XX

SQ Sequence 927 AA;

Query Match 97.7%; Score 4686; DB 5; Length 927;
 Best Local Similarity 96.8%; Pred. No. 0;

Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      |||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRKKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      |||:|||||:|||||
Db    181 IIGICVYVIPDGETRKKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      |||:|||||:|||||
Db    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGEHKPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR 360
      |:|||||
Db    301 LIPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||:|||||
Db    361 MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDI FEEDEHF 480
      |||:|||||
Db    421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDI FEEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||:|||||
Db    481 FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600
      |||
Db    541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600

Qy    601 KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPVL 654
      |||:|||||
Db    601 KIVDEEEYERQENFFIALGEPKWMERGISALLSPEVTDKLTMEEEEAKRIAEMGKPVL 660

Qy    655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
      |||:|||||:|||||
Db    661 GEHPKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDESG 720

Qy    715 EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 774
      |||
Db    721 EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFVVSILIIIGMLTAIIGDLASHFG 780

Qy    775 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
      |||
Db    781 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 840
```

Qy 835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
 |||||:|||||:|||||:|||||:|||||
 Db 841 SVAAIYWAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLA 900
 Qy 895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||||:|||||
 Db 901 TTWLFVSLWLLYVLFATLEAYCYIKGF 927

RESULT 9

ABU12042

ID ABU12042 standard; protein; 925 AA.

XX

AC ABU12042;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1b CG56558-02 protein SEQ ID 4.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.

XX

OS Homo sapiens.

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PN WO200281625-A2.

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PD 17-OCT-2002.

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PF 03-APR-2002; 2002WO-US010366.

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PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.
PR 03-JAN-2002; 2002US-0345755P.
PR 04-FEB-2002; 2002US-0354391P.
PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR N-PSDB; ABX56262.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 1; Page 85; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

XX

SQ Sequence 925 AA;

Query Match 97.4%; Score 4671; DB 6; Length 925;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 896; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
|||||

Db 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
|||||

Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETIVKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETIVKTIHI	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGE	656
		::: ::: ::: ::: ::: ::: ::: ::: :::	
Db	601	KVIDDEAYEKNKNYFIEMMGPRMVDMSFQKALLSPDRKLTMEEEEAKRIAEMGKPVLGE	660
Qy	657	HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE	716
Db	661	HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE	720
Qy	717	RLPSCFDYVMHFLTTFWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCT	776
Db	721	RLPSCFDYVMHFLTTFWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCT	780
Qy	777	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSV	836
Db	781	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSV	840
Qy	837	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGEELGGPRGCKLATT	896
Db	841	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGEELGGPRGCKLATT	900
Qy	897	WLFVSLWLLYILFATLEAYCYIKGF	921
Db	901	WLFVSLWLLYILFATLEAYCYIKGF	925

RESULT 10

ABU12043

ID ABU12043 standard; protein; 895 AA.

XX

AC ABU12043;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 protein SEQ ID 6.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR N-PSDB; ABX56263.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 1; Page 86; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

XX

SQ Sequence 895 AA;

Query Match 96.8%; Score 4644; DB 6; Length 895;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 891; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      30 AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 89
      :|||||
Db      2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61

Qy     90 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 149
      :|||||
Db     62 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 121

Qy    150 LSLIEVCGHGFIAGDLGPSTIVGSAAFMFIIIGICVYVIPDGETRRIKHLRVFFITA AW 209
      :|||||
Db    122 LSLIEVCGHGFIAGDLGPSTIVGSAAFMFIIIGICVYVIPDGETRRIKHLRVFFITA AW 181

Qy    210 SIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK 269
      :|||||
```

Db	182	SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK	241
Qy	270	HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	329
Db	242	HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	301
Qy	330	KDLDQLVEMANYYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	389
Db	302	KDLDQLVEMANYYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	361
Qy	390	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT	449
Db	362	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT	421
Qy	450	EGTVVLKPGETQKEFSVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	509
Db	422	EGTVVLKPGETQKEFSVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	481
Qy	510	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	569
Db	482	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	541
Qy	570	EGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	629
Db	542	EGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	601
Qy	630	DVTDRLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVG	689
Db	602	DVTDRLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVG	661
Qy	690	HSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWKVL FACVPPTEYCHGW	749
Db	662	HSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWKVL FACVPPTEYCHGW	721
Qy	750	ACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	809
Db	722	ACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	781
Qy	810	YADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFC	869
Db	782	YADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFC	841
Qy	870	ISVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	921
Db	842	ISVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	893

RESULT 11

ABU12041

ID ABU12041 standard; protein; 928 AA.

XX

AC ABU12041;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1a CG56258-01 protein SEQ ID 2.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
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OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

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PF 03-APR-2002; 2002WO-US010366.

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PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

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PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

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PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;

PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;

PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR N-PSDB; ABX56261.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||

Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||

Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
 |||

Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTLQV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPV 654
 |||:||||:|||| |||:||||: ||| : ||| |||:|||||

Db 601 KIVDDEEYKKNDFNFFIELGQPQWLKRGISALLNQGDGRKLTAEEEEARRIAEMGKPV 660

Qy 655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
 ||: :|||||:| |||:|||||:|||||:|:|||| | |||:|:|

Db 661 GENCRLEVIIIEESYDFKNTVDKLIKKTNLALVIGTHSWREQFLEAITVS-AGDEEEEDG 719

Qy 715 --EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIGMLTAIIGDLASH 772
 |||

Db 720 SREERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFGVSILVIGLLTALIGDLASH 779

Qy 773 FGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGL 832
 |||:|||| | ||| |||:|||| | ||| |||

Db 780 FGCTVGLKDSVNAVVFVALGTSIPDTFASKVAALQDQCADASIGNVTGSNAVNVLGLGV 839

Qy 833 AWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCK 892
 |||:||||:|:| | ||| |||:|||| | |||:||||:||||| |

Db 840 AWSVAAVYWAVQGRPFVVRTGTAFSVTLFTVFVAFVGIALLYRRRPHIGGELGGPRGPK 899

Qy 893 LATTWLFVSLWLLYILFATLEAYCYIKGF 921
 ||| ||: |||:|||||:||||:|:|

Db 900 LATTALFLGLWLLYILFASLEAYCHIRGF 928

RESULT 12

AAE18291

ID AAE18291 standard; protein; 970 AA.

XX

AC AAE18291;

XX

DT 07-MAY-2002 (first entry)

XX

DE Bovine NCX-1 protein.

XX

KW Bovine; recombinant protein; larvae expression system; membrane protein;
 KW transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
 KW NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
 KW channel forming protein; junctional protein; connexin 32.

XX

OS Bos taurus.

XX

PN WO200206464-A2.

Db 177 FIIIALCVYVVPDGETRKHILRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF 236

Qy 239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGII IETEGDHPKG---IEMDGKMMNSH 295
 ||||:|: ||||:||||||:|:| | ||:| | | | ||||:| |

Db 237 FFFPICVVFVAVDRRLLFYKYVYKRYRAGKQGRMI IEHEGDRPSSKTEIEMDGKVVNSH 296

Qy 296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYALSHQQ 348
 |||| | | | | | | :||| ||||:||||||:|:|:|:| | | |

Db 297 VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy 349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQC 407
 |||||:|||||:|||||:|:|:| | | | | | :|:| | :| |

Db 356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTVAENDPVSKI FFEQGTQC 415

Qy 408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 |||| | | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| |

Db 416 LENC GTVALTI IRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | | | |:| | |:| | | | | | | | | | | |

Db 476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| | | | | | | | | | | | | | | | | | | | | | | |

Db 533 HAGIFTFEFPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy 588 EFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERG----- 627
 |:| | | | | | |:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 593 EFQND EIVKTISVKVIDDEEYEKNKTFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL 652

Qy 628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVI 663
 |:| | | | | | |:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 653 YGQPVFRKVHAREHPLPSTIITIAD EYDDKQPLTSKEEEEERRIAEMGRPILGEHTRLEVI 712

Qy 664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD 723
 |||||:|||||:|||||:|:|:|:|:|:| | |:| | | |:| |

Db 713 IEESYEFKSTVDKLIKKTNLALVVG TNSWREQFIEAITVSAGEDDDDDDECGEELPSCFD 772

Qy 724 YVMHFLT VFWKVLFA CVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSV 783
 ||||| | | | | | | | | | | | | | | | | | | | | | | |

Db 773 YVMHFLT VFWKVLFAFVP PTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV 832

Qy 784 TAVVFVAFGTSVPD TFAKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA AIYWAL 843
 ||||| | | | | | | | | | | | | | | | | | | | | | |

Db 833 TAVVFVALGTSVPD TFAKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIA AIYHAA 892

Qy 844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLG GELGGPRGCKLATTWLFVSLW 903
 |:| | | | | | | | | | |:| | | | | | | | | | | | |

Db 893 NGEQFKVSPGTLAFSVTLFTIFAFINVG VLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 952

Qy 904 LLYILFATLEAYCYIKGF 921
 |||| |:| | | | |:| | |

Db 953 LLYIFFSSLEAYCHIKGF 970

ID AAO27170 standard; protein; 921 AA.
XX
AC AAO27170;
XX
DT 02-SEP-2003 (first entry)
XX
DE Human 46566 protein (Na-Ca exchanger SLC8).
XX
KW Na-Ca exchanger SLC8; 46566; hyperalgesia; allodynia; nociceptive;
KW analgesic; neuropathic; fibromyalgia; migraine; arthritis; causalgia;
KW chronic fatigue syndrome; neurodystrophy; plantar fasciitis; pain; human.
XX
OS Homo sapiens.
XX
PN WO2003037254-A2.
XX
PD 08-MAY-2003.
XX
PF 28-OCT-2002; 2002WO-US034567.
XX
PR 31-OCT-2001; 2001US-0335078P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Silos-Santiago I;
XX
DR WPI; 2003-457344/43.
DR N-PSDB; AAL55587.
XX
PT Identifying compounds that modulate 46566 (Na-Ca exchanger SLC8) nucleic
PT acid expression or polypeptide activity, useful for preventing and
PT treating pain disorders e.g. inflammatory, chronic, neuropathic and
PT cancer pain.
XX
PS Disclosure; Fig 1b; 74pp; English.
XX
CC This invention relates to novel methods and compositions for the
CC diagnosis and treatment of pain disorders. The Na-Ca exchanger SLC8
CC referred to herein as 46566, is predominantly expressed in the nervous
CC tissues (brain, spinal chord and dorsal root ganglia). Furthermore, it is
CC down-regulated in animal models of pain such that there is an altered
CC pain response, which manifests as a reduced threshold to noxious stimuli
CC (hyperalgesia) and lowered thresholds to innocuous stimuli (allodynia).
CC Therefore the 46566 molecule is believed to be involved in nociceptive
CC pathways by participating in pain signalling mechanisms and modulating
CC pain elicitation, hence it provides a target by which to control pain and
CC treat disorders. This invention provides methods to identify analgesic
CC compounds that modulate 46566 expression or 46566 activity and
CC consequently are capable of treating inflammatory, chronic and/ or
CC neuropathic pain. It further provides diagnostic assays, as well as
CC prophylactic and therapeutic methods for treating subjects with, for
CC example, fibromyalgia, cancer pain, chronic fatigue syndrome, migraine
CC pain, arthritis, causalgia, neurodystrophy or plantar fasciitis. This
CC polypeptide sequence is the human 46566 protein sequence (Na-Ca exchanger
CC SLC8) of the invention
XX
SQ Sequence 921 AA;

Query Match 70.3%; Score 3373.5; DB 7; Length 921;
Best Local Similarity 71.0%; Pred. No. 0;
Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;

Qy	40	STGQNNESCSGSSDCKEGLVLPWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFM	99
Db	39	STG----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIADRFM	94
Qy	100	ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG	159
Db	95	AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN	154
Qy	160	FIAGDLGPSTIVGSAAAFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYM	219
Db	155	FQAGELGPGTIVGSAAAFNMVVIACVIYPAGESRRIKHLRVFFVTASWSIFAYVWLYL	214
Qy	220	ILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEG	279
Db	215	ILAVFSPGVVQVWEALLTLVFFPVCVVFAMVADKRLLFYKYVYKRYRTDPRSGIIIGAEG	274
Qy	280	DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRILKDLKQKHPEKDLQ	334
Db	275	DPPKSIELDGTGTFVGAEL-APGELGGLGPGPAEARELDASRREVIQILKDLKQKHDPKDLQ	333
Qy	335	LVEMANYYALSHQKQSRAFYRIQATRMMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDF	394
Db	334	LVGIANYYALLHQKQSRAFYRIQATRLMTGAGNVLRRAADASRRAPAEAGAGEDE-DDG	392
Qy	395	ISKVFFDPCSQYQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVV	454
Db	393	ASRIFFEPSLYHCLNCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDYEYSEGLTV	452
Qy	455	LKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR	510
Db	453	FKPGETQKELRIGIIDDDIFEEDHFFVRLNLNRVGDAQGMFEPDGG-----GRPK	503
Qy	511	AVLASPCVATVTILDDDHAGITFECDTIHVSESIGVMEVKVLRVTSARGTVIVPFRTVE	570
Db	504	GRLVAPLLATVTILDDDHAGIFSFDRLHVSCEMGTVDVRVVRSSGARGTVRLPYRTVD	563
Qy	571	GTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGISD	630
Db	564	GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYKKNDFFIELGQPQWLKRGISA	623
Qy	631	VT-----DRKLTMEEEEAKRIAEMGKPVLGHPKLEVIIEESYEFKTTVDKLIKKTNLA	684
Db	624	LLNQGDGDRKLTAEIEEEARRIAEMGKPVLGENCRLVIIEESYDFKNTVDKLIKKTNLA	683
Qy	685	LVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHFLT VFWKVLFAVPP	742
Db	684	LVIGTHSWREQFLEAITVS-AGDEEEEDGSREERLPSCFDYVMHFLT VFWKVLFAVPP	742
Qy	743	TEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK	802
Db	743	TEYCHGWACFGVSILVIGLLTALIGDLASHFGCTVGLKDSVNAVVFVALGTSIPDTFASK	802

Qy 803 AAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF 862
 Db 803 VAALQDQCADASIGNVTGSNAVNVLGGLGVAWSVAAVYWAVQGRPFVVRTGTALAFSVTLF 862

Qy 863 TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
 Db 863 TVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWLLYILFASLEAYCHIRGF 921

RESULT 14

AAB41497

ID AAB41497 standard; protein; 952 AA.

XX

AC AAB41497;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human ORFX ORF1261 polypeptide sequence SEQ ID NO:2522.

XX

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200058473-A2.

XX

PD 05-OCT-2000.

XX

PF 31-MAR-2000; 2000WO-US008621.

XX

PR 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach M;

XX

DR WPI; 2000-602362/57.

DR N-PSDB; AAC75706.

XX

PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

XX
PS Claim 11; Page 1809-1812; 5507pp; English.

SQ Sequence 952 AA;

Qy	40	STGQNNESCSGSSDCKEGLVLPWIYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM	99
Db	70	STG----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM	125
Qy	100	ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG	159
Db	126	AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN	185
Qy	160	FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYM	219
Db	186	FQAGELGPGTIVGSAAFNMFVVIACIYVIPAGESRRIKHLRVFFVTASWSIFAYVWLYL	245
Qy	220	ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEG	279
Db	246	ILAVFSPGVVQVWEALLTLVFFPVCVVFAMWADKRLLFYKYVYKRYRTDPRSGIIIGAEG	305
Qy	280	DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRILKDLKQKHPEKDLQ	334
Db	306	DPPKSIELDGTFTVGAE-APGELGGLGPGPAEARELDASRREVIQILKDLKQKHDPKDLEQ	364
Qy	335	LVE MANY YALSHQQKSRAFYRIQATRMMTGAGN ILKKHAAEQAKKASSMSEVHTDEPEDF	394
Db	365	LVGIANY YALLHQQKSRAFYRIQATRLMTGAGNVLRRHAADASRRAPAEGAGEDE-DDG	423
Qy	395	ISKVFFDPCS YQCLENC GAVLLTVVRKGGDMSKTM YVDYKTEDGSANAGADYEFTEGTVV	454
Db	424	ASRIFFEPSLYHCLENC SVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDY EYSEGTLV	483

XX
PA (MILL-) MILLENIU PHARM INC.
XX
PI Carroll JM;
XX
DR WPI; 2003-381617/36.
DR N-PSDB; ACC00414.
XX
PT Identifying a nucleic acid molecule associated with a disorder for
PT preparing a composition for treating hematopoietic or neurological
PT disorder by detecting the presence of a nucleic acid molecule in the
PT sample that is amplified.
XX
PS Example 1; Page 110; 133pp; English.
XX
CC The present sequence is the protein sequence for human 69039, a novel
CC Na⁺/Ca²⁺ exchanger family member (ion transporter). 69039 was shown to be
CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder
XX
SQ Sequence 595 AA;

Query Match 64.5%; Score 3093; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 4.9e-294;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120	
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120	
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180	
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180	
Qy	181	IIGICVYVIPDGETRKHKL	RVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHKL	RVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYM	HKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYM	HKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRR	EMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRR	EMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENC	GAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENC	GAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480	


```

Db .      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Search completed: June 24, 2004, 16:11:56
 Job time : 67.95 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:09:57 ; Search time 23.3089 Seconds
(without alignments)
2039.888 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	579	12.1	539	4	US-09-701-068-2	Sequence 2, Appli
2	506	10.5	474	4	US-09-701-068-5	Sequence 5, Appli
3	128.5	2.7	693	4	US-09-564-805-234	Sequence 234, App
4	128.5	2.7	4654	3	US-08-476-515A-84	Sequence 84, Appl
5	128.5	2.7	4655	3	US-08-652-877-84	Sequence 84, Appl
6	128.5	2.7	4655	3	US-08-652-877-86	Sequence 86, Appl
7	128.5	2.7	4655	3	US-08-652-877-88	Sequence 88, Appl
8	128.5	2.7	4655	3	US-08-652-877-90	Sequence 90, Appl
9	121	2.5	325	4	US-09-489-039A-13618	Sequence 13618, A
10	116	2.4	355	4	US-09-543-681A-5929	Sequence 5929, Ap
11	115.5	2.4	1786	3	US-08-973-462-8	Sequence 8, Appli

12	115.5	2.4	1805	1	US-07-853-913-2	Sequence 2, Appli
13	113.5	2.4	339	4	US-09-134-001C-3608	Sequence 3608, Ap
14	111	2.3	660	4	US-09-134-001C-3350	Sequence 3350, Ap
15	111	2.3	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
16	110.5	2.3	720	4	US-09-708-426-8	Sequence 8, Appli
17	109.5	2.3	1144	3	US-08-726-214-6	Sequence 6, Appli
18	108.5	2.3	652	1	US-08-050-684-2	Sequence 2, Appli
19	108.5	2.3	652	1	US-08-582-719-2	Sequence 2, Appli
20	108	2.3	721	4	US-09-134-078-19	Sequence 19, Appl
21	108	2.3	986	4	US-08-311-731A-2	Sequence 2, Appli
22	106.5	2.2	501	4	US-09-489-039A-9817	Sequence 9817, Ap
23	106.5	2.2	1780	1	US-08-769-309A-5	Sequence 5, Appli
24	106.5	2.2	1780	3	US-08-994-570-5	Sequence 5, Appli
25	106.5	2.2	2954	4	US-09-150-867-1	Sequence 1, Appli
26	105.5	2.2	480	2	US-08-962-203-2	Sequence 2, Appli
27	105.5	2.2	480	3	US-09-282-125A-2	Sequence 2, Appli
28	105.5	2.2	480	4	US-09-273-142-2	Sequence 2, Appli
29	105.5	2.2	3878	4	US-09-914-259-11	Sequence 11, Appl
30	105	2.2	404	4	US-09-198-452A-718	Sequence 718, App
31	105	2.2	1028	4	US-09-328-352-5749	Sequence 5749, Ap
32	104	2.2	1432	3	US-08-781-891-71	Sequence 71, Appl
33	104	2.2	1432	4	US-09-618-166-71	Sequence 71, Appl
34	103.5	2.2	988	2	US-08-286-819A-19	Sequence 19, Appl
35	103.5	2.2	988	3	US-08-980-357-19	Sequence 19, Appl
36	103.5	2.2	1451	4	US-09-060-299-25	Sequence 25, Appl
37	103.5	2.2	1451	4	US-09-402-923A-25	Sequence 25, Appl
38	103.5	2.2	1584	4	US-09-060-299-39	Sequence 39, Appl
39	103.5	2.2	1584	4	US-09-402-923A-39	Sequence 39, Appl
40	103.5	2.2	1591	4	US-09-060-299-4	Sequence 4, Appli
41	103.5	2.2	1591	4	US-09-060-299-43	Sequence 43, Appl
42	103.5	2.2	1591	4	US-09-402-923A-4	Sequence 4, Appli
43	103.5	2.2	1591	4	US-09-402-923A-43	Sequence 43, Appl
44	103.5	2.2	1615	4	US-09-060-299-3	Sequence 3, Appli
45	103.5	2.2	1615	4	US-09-402-923A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-701-068-2

; Sequence 2, Application US/09701068

; Patent No. 6677506

; GENERAL INFORMATION:

; APPLICANT: Galil, Gad et al.

; TITLE OF INVENTION: DNA CODING FOR A Mg²⁺/H⁺ OR Zn²⁺/H⁺ EXCHANGER AND
TRANSGENIC PLANTS

; TITLE OF INVENTION: EXPRESSING SAME

; FILE REFERENCE: 01/21317

; CURRENT APPLICATION NUMBER: US/09/701,068

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 539

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

Query Match 12.1%; Score 579; DB 4; Length 539;
 Best Local Similarity 22.3%; Pred. No. 5.7e-48;
 Matches 191; Conservative 110; Mismatches 199; Indels 356; Gaps 22;

```

Qy      64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST 123
      :|  :|  | : | :||: | | |:| | | | |:| :  |:|  | :
Db      29 FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV 87

Qy     124 TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF 179
      | :||| |:::|:| | :| | : | :  | : || || | :||| |:::|
Db      88 ITYKKVWNFTIADISLLAFGTSFPQISLATIDAIRNMGERY-AGGLGPGTLVGSAAFDLF 146

Qy     180 IIIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF 239
      | :|| |  || :|| | | : :  || :||| |:::| | :|| | : : | ||:
Db     147 PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL 206

Qy     240 FFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
      : : : : |: |||  : |:  : : || |:
Db     207 QYGLLLVHAYAQDKR---WPYLS-----LPMRGRDRPE----- 236

Qy     300 NLVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVLVEMANYYALSHQKSRIFYRIQAT 359
      ||  :|| | :  : | |
Db     237 EWVP---EEIDTSK-----DDNDND----- 253

Qy     360 RMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCS YQCLENCGAVLLTVV 419
      : : ||:| : | :
Db     254 -----VHDVYSDAQAQDAV----- 266

Qy     420 RKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEH 479
      | || |  | :|
Db     267 -----ESGRN-----IVD----- 275

Qy     480 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTI 539
      | |  :|
Db     276 -----IF-----SI 279

Qy     540 HVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGEDFEDTYGELEFKNDETVKTIR 599
      |  : : || |  | | :
Db     280 H-----SANNDTGITYHTVADTPP-----DSATKKGK 306

Qy     600 VKIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHEPK 659
      |
Db     307 AK----- 308

Qy     660 LEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLP 719
      :|| :  | : ||:| | : : | | |:
Db     309 -----NSTVFDI-----WKHQFVDAITLETSESKKVD-SIYLRIA 342

Qy     720 SCFDYVMHFLT VFWKVL FACVPPT EYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGL 779
      |  | | | :||| |||  || | |:| | : :  | | :
Db     343 KSF---WHLLLAPWKLLFAFVPPCNIAHGWI AFICSLLFISGVA FVVTRFTDLISCVTGI 399

Qy     780 KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA AI 839
      | |  : | || | | | | : : | : ||:| | : ||:| :||:| : | :
Db     400 NPYVIAFTALASGTSWPD LVASKIAAERQLTADSAIANITCSNSVNIYVGIGVPWLINTV 459

```


Qy 454 VLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVL 513
 Db 208 -----IVD----- 210
 Qy 514 ASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTA 573
 Db 211 -----IF-----SIH-----SANNDTGITYHTVADTP 232
 Qy 574 KGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGISDVTD 633
 Db 233 P-----DSATKKGKAK----- 243
 Qy 634 RKLTMEEEEAKRIAEMGKPV LGEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWR 693
 Db 244 -----NSTVFDI-----WK 252
 Qy 694 DQFMEAITVSAAGDEDEDES GEERLPSCFDYVMHFLT VFWKVL FACVPPTEYCHGWACFA 753
 Db 253 HQFVDAITVKIFNLPKVD-SIYLRIAKSF--WHLLAPWKLLFAFVPPCNIAHGWI AFI 308
 Qy 754 VSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADA 813
 Db 309 CSLLFISGVAFVVT RFTDLISCVTGINPYVIAFTALASGTSWPD LVASKIAAERQLTADS 368
 Qy 814 SIGNVTGSNAVNVFLGIGLAWSVAAI--YWALQGQEFHVSAGTLAFSVTLFTIFAFVCIS 871
 Db 369 AIANITCSNSVNIYVGIGVPWLINTVYNYFAYREPLYIENAKGLSFSLLIFFATSVGCIV 428
 Qy 872 VLLYRRRPHLG GELGGPRGCKLATTWLFVSLWLLYILFATLE 913
 Db 429 VLVLRRRL-IIGAELGGPRLWAWLTSAYFMMLWVVFVVLSSLK 469

RESULT 3

US-09-564-805-234

; Sequence 234, Application US/09564805

; Patent No. 6333403

; GENERAL INFORMATION:

; APPLICANT: Tavtigian, Sean V.

; APPLICANT: Teng, David H.F.

; APPLICANT: Simard, Jacques

; APPLICANT: Rommens, Johanna M.

; APPLICANT: Myriad Genetics, Inc.

; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

; FILE REFERENCE: 2318-258

; CURRENT APPLICATION NUMBER: US/09/564,805

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: US 60/107,468

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: 09/434,382

; PRIOR FILING DATE: 1999-11-05

; NUMBER OF SEQ ID NOS: 240

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 234

; LENGTH: 693

; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-564-805-234

Query Match 2.7%; Score 128.5; DB 4; Length 693;
Best Local Similarity 19.6%; Pred. No. 0.0031;
Matches 132; Conservative 88; Mismatches 206; Indels 249; Gaps 32;

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Qy      153 IEVCGHGFIAAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKLRFVFFITAAWSIF 212
      :|| | | | :||:| | | | : : | : :|||
Db      154 VEVNGIKFWCYTAG--HVLGAAMF-MVDIAGVRILYTDGYSREEDRHLRA----- 200

Qy      213 AYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRG 272
      | ||| :||: : : :| :||:| ||
Db      201 -----AELPQFSP-----DICIIES-TSGVQLHQSRHIREKRFTD---- 234

Qy      273 IIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEKDL 332
      :| | : ||: | | :||: || : ||:
Db      235 VIHST-----VAQGGRVLI PAFALGR-----AQELLLILDEYWANHPD--- 272

Qy      333 DQLVEMANYIALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE 392
      | : ||| :| | : | | | | : : :
Db      273 --LHNIPIYYASPLAKKCMAVYQTYILSMNDRIRNQFANSNPFVKHISPLNSI-----D 325

Qy      393 DF-----ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKT----- 428
      || :|| | : | : | :||
Db      326 DFNDVGPSVVMATPGGLQSGLSRQLFDS---WCSDKKNACIIPGYMVEGTLAKTIINEPK 382

Qy      429 -----MYVDYKTEDGSANAGADY-----EFTEGTVVLKPGETQK----- 462
      | | | | :||| | :|| :
Db      383 EVTLMNGLTAPLNMQVHYI----SFSAHADYAQTSTFLKELMPPNIILVHGEANEMMLRK 438

Qy      463 -----EFSVG---IIDDDIFEEDHFF--VRLSNV--RIEEEQPEEGMPPAIFNSLPLPR 510
      || | : | | :| :| :| :| :|
Db      439 QKLLTEFPDGNTKIMTPKNCESVEMYFNSEKLAKTIGRLAEKTPDVG----- 485

Qy      511 AVLASPCVATVTILDDDHAGI-----FTFEC---DTIHVSESIGVMEVKVLRTSGARGTV 562
      | :|| ||: | :|| | | :
Db      486 -----DTVSGILVKKGFTYQIMAPDELHVFSQ-----LSTATVTQRI 522

Qy      563 IVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPK 622
      :|| | | | : :|| || : : : :| :
Db      523 TIPFVGAFGVK---HRLEKIFESVEFSTDEESGLPALKVHERVTVKQESEKHISL---Q 576

Qy      623 WMERGISD-VTDR-----KLTMEEEEA-KRIAEMGKPV----- 653
      | ||| :| : ||||:| | | |||
Db      577 WSSDPISDMVSDSIVALILNISREVPKIVMEEEDAVKSEEENGKKVEKVIYALLVSLFGD 636

Qy      654 --LGEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDED 711
      |||: || : : : | :| : :||: :
Db      637 VKLGENGKLVIRVDGN-----VAQLDKE-----SGEVESE 666

Qy      712 ESG-EERLPSCFDYV 725
      || :||: | :
Db      667 HSGLKERVVAFERI 681
```

RESULT 4

US-08-476-515A-84

; Sequence 84, Application US/08476515A

; Patent No. 6239270

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Martin Savitzky

; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;

; STREET: 3C43,

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 7.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,515A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE94/00483

; FILING DATE: 24-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9301764-8

; FILING DATE: 24-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4654 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-476-515A-84

Query Match

2.7%; Score 128.5; DB 3; Length 4654;

Best Local Similarity 18.4%; Pred. No. 0.087;
Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;

```

Qy      156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHL----- 200
      | |:: | : | :: :: :: : | | | :: ::
Db      1415 CDTGYMLES DGRTCKV-TASESLLLLLVASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDF 1473

Qy      201 -----RVFFITA----AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVA 251
      | :: | | | : | | : : : : | |
Db      1474 DSISGRIFWSDATQGKTWSAFQNGTDRRV--VFDSSII-----LTETIAIDWVG 1520

Qy      252 DKRLLFYKYMHHKYRTDK---HRGIIIETEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
      : | : | : | | | :: | : | : | : | | | | :
Db      1521 -RNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSDWGHHPR 1578

Qy      304 LEGKEVDESREMI-----RIL-----K 321
      : | : | | : | | : |
Db      1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMDFCDYNGHRRQVIAS 1638

Qy      322 DLKQKHPEKDLQVLVEMANYIALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS 381
      | | : | | | | : | : | : | : | | | :
Db      1639 DLIIRHP-----YALTLFEDS-VYWTD RATRRVMRAN---KWHGGNQSVVMY 1681

Qy      382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-----LENC- 411
      : : | | : : : | | : | | |
Db      1682 NIQWPLGIVAVHPSKQPN SVNPCAFSRCSHLCLLSSQGP HFYSCVCPSGWSLSPDLLNCL 1741

Qy      412 --GAVLLTVVRKGGDMSKTMVVDYKTED-----GSANAGADYEFTEGTV---VLKPGE 459
      | | | : : : : | | | | | : | | |
Db      1742 RDDQPFLITVRQHIIIFGISLNPEVKSNDAMVPIAGIQN-GLDVEFD DAEQYIYWVENPGE 1800

Qy      460 TQKEFSVGIIDDDIFEED EHFVRLSNVRIEEEQPEEGMPPAIFNSLPL--PRAVLASPC 517
      : : | : | : | |
Db      1801 IHR-----VKTDG TNRTVFASISMGPSMNLA--- 1827

Qy      518 VATVTILDDDHAGIFTFEC DTIHVSESIGVMEVKVLR TSG---ARGTVIVPFRTVEGTAK 574
      | | : : | : : | | | | | : | | |
Db      1828 -----LDWISRNLY-----STNPRTQSIEVLT LHGDIRYKRTL IAN---DGTAL 1868

Qy      575 GGGEDF----EDTYGELEFKNDET VKTIRVKIVDEE-----EY 608
      | | : | : : | : |
Db      1869 GVGFPIGITVDPARGKLYWSDQGTDSGVP AKIASANMDGTSVKTLFTGNLEHLEC VTLDI 1928

Qy      609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES 667
      | | : : | : | | | : : : | : | : |
Db      1929 EEQKLYWAVTGRGV-IERGNVDG TDRMIL-----VHQLSHPWGIAVHDSFLY YTTDEQ 1979

Qy      668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDES GEERLPSCFDYV 725
      | | | | : | | : : | : | : | : :
Db      1980 YEVI ERVDKATGANKIVL-----RDNV PNLRGLQVYHRRNAAESSNG-----CSNNM 2026

Qy      726 MHFLT VFWKV---LFACV-----PPTEYCHGWACFAVSILIIGMLTAIIG---DLAS 771
      : | | | | | : | : | : | : | :
Db      2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLS AIRGFSLELSD 2082

Qy      772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT---- 819
      | : : : : | | | | : | | : : | : :

```

Db 2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142
Qy 820 GSNVNVFLGIGLAWSVAIYW 841
| | | | : | : |
Db 2143 GENGV---GIAVDWVAGNLYF 2161

RESULT 5

US-08-652-877-84

; Sequence 84, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalm, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4655 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-877-84

Query Match 2.7%; Score 128.5; DB 3; Length 4655;
Best Local Similarity 18.4%; Pred. No. 0.087;
Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;

```
Qy      156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKL----- 200
      | |:: | : | :: :: :: : | | | :: ::
Db      1415 CDTGYMLES DGRTCKV-TASESLLLLVASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDF 1473

Qy      201 -----RVFFITA----AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVA 251
      | :: | | | : | | :: : : : | | : : | |
Db      1474 DSISGRIFWSDATQGKTWSAFQNGTDRRV--VFDSSII-----LTETIAIDWVG 1520

Qy      252 DKRLLFYKYMHHKYRTDK---HRGIIETEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
      : | : | : | | | :: | : :: : : | : | | | | :
Db      1521 -RNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSDWGHHPR 1578

Qy      304 LEGKEVDESRRMI-----RIL-----K 321
      : | : | | : | | : |
Db      1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMDFCDYNGHRRQVIAS 1638

Qy      322 DLKQKHPEKDLQLVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS 381
      || : || | | : : | : : || : | | | :
Db      1639 DLIIRHP-----YALTLFEDS-VYWTD RATRRVMRAN---KWHGGNQSVVMY 1681

Qy      382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-----LENC- 411
      : : | | : : : | | : | | |
Db      1682 NIQWPLGIVAVHPSKQPN SVNPCA FSRCSHLCLLSSQGP HFYSCVCPSGWSLSPDLLNCL 1741

Qy      412 --GAVLLTVVRKGGDMSKTMVVDYKTED-----GSANAGADYEFTEGTV---VLKPGE 459
      | || : : : : | | | | | : | ||
Db      1742 RDDQPFLITVRQHIIFGISLNPEVKSN DAMVPIAGIQN-GLDVEFD DAEQYIYWVENPGE 1800

Qy      460 TQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL--PRAVLASPC 517
      : : : : : | : : : | |
Db      1801 IHR-----VKTDG TNRTVFASIS MVGPS MNLA--- 1827

Qy      518 VATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLR TSG--ARGTVIVPFRTVEGTAK 574
      || : : | : : || | | : | : ||
Db      1828 -----LDWISRNLY-----STNPRTQSIEVLT LHGDIRYRKT LIAN----DGTAL 1868

Qy      575 GGGEDF----EDTYGELEFKNDET VKTIRVKIVDEE-----EY 608
      | | : | : : | : | :
Db      1869 GVGFPIGITVDPARGKLYWSDQGTDSGVP AKIASANMDGTSVKTLFTGNLEHLEC VTLDI 1928

Qy      609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES 667
      | | : : | : || | || : : : | : | :
Db      1929 EEQKLYWAVTG RGV-IERGNVDGTD RMIL-----VHQLSHPWGI AVHDSFLYYTDEQ 1979

Qy      668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDES GEERLPSCFDYV 725
      || || : | | : : | : | : | : :
Db      1980 YEVIERVDKATGANKIVL-----RDNP NLRGLQVYHRRNAAESSNG-----CSNNM 2026
```

Qy 726 MHFLT VFWKV---LFACV-----PPTEYCHGWACFAVSILIIGMLTAIIG---DLAS 771
 : | ||: | | : | : : ||: || | : :
 Db 2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLSAIRGFSLELS 2082

Qy 772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT----- 819
 | : : : : | : | | : | | : : | : : | :
 Db 2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCD FSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142

Qy 820 GSNAVNVFLGIGLAWSVA AIYW 841
 | | | | : | : :
 Db 2143 GENGV R---GIAVDWVAGNLYF 2161

RESULT 6

US-08-652-877-86

; Sequence 86, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalm, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4655 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-877-86

```

```

Query Match          2.7%; Score 128.5; DB 3; Length 4655;
Best Local Similarity 18.4%; Pred. No. 0.087;
Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;

```

```

Qy      156 CGHGFIAGDLGPSTIVGSAAFNMIIIGICVYVIPDGETRKIKHL----- 200
      | |:: | : | :: :: :: : | | | :: ::
Db      1415 CDTGYMLES DGRTCKV-TASESLLLLVASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDF 1473

Qy      201 -----RVFFITA----AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVA 251
      |:: | | | | : | | : : | | : : | |
Db      1474 DSISGRIFWSDATQGKTWSAFQNGTDRRV--VFDSSII-----LTETIAIDWVG 1520

Qy      252 DKRLLFYKYMHKKYRTDK----HRGIIETEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
      : | : | : | | | :: | : :: : | : | | | | :
Db      1521 -RNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSWDWGHHPR 1578

Qy      304 LEGKEVDESREMI-----RIL-----K 321
      : | : | | | : | | : |
Db      1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMFCDYNGHHRRQVIAS 1638

Qy      322 DLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS 381
      || : || | | : : | : : || : | | | :
Db      1639 DLIIRHP-----YALTLFEDS-VYWTDRA TRRVMRAN---KWHGGNQSVVMY 1681

Qy      382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-----LENC- 411
      :: | : : : : | | : | | |
Db      1682 NIQWPLGIVAVHPSKQPNVNPACAFSRCSHLCLLSSQGPHFYSCVCPGWSLSPDLLNCL 1741

Qy      412 --GAVLLTVVRKGGDMSKTMVVDYKTED-----GSANAGADYEFTEGTV---VLKPGE 459
      | || : : : : | | | | | : | ||
Db      1742 RDDQPFLITVRQHIIIFGISLNPEVKSNDAMVPIAGIQN-GLDVEFDDAEQYIYWVENPGE 1800

Qy      460 TQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL--PRAVLASPC 517
      : : | : | : : | |
Db      1801 IHR-----VKT DGTNRTVFASISMVGPSMNLA--- 1827

Qy      518 VATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLR TSG---ARGTVIVPFRTVEGTAK 574
      || : : | : : || | | : | |
Db      1828 -----LDWISRNLY-----STNPRTQSIEVLT LHGDIRYKRLIAN----DGTAL 1868

Qy      575 GGGEDF----EDTYGELEFKNDETVKTIRVKIVDEE-----EY 608
      | | : | : : | : |
Db      1869 GVGFPIGITVDPARGKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTGNLEHLEC VTLDI 1928

Qy      609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIIES 667
      | | : : | : || | || : : : | : | : |

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Db 1929 EEQKLYWAVTGRGV-IERGNVDGTDRLMIL-----VHQLSHPWGIHAVHDSFLYYTDEQ 1979

Qy 668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDESGEERLPSCFDYV 725
 || ||| : | || : : | : | : :
 Db 1980 YEVIERVDKATGANKIVL-----RDNVPNLRGLQVYHRRNAAESSNG-----CSNNM 2026

Qy 726 MHFLTTFWKV---LFACV-----PPTYCHGWACFAVSILIIIGMLTAIIG---DLAS 771
 : | ||: | | : | : : ||: || | : :
 Db 2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLSAIRGFSLELSD 2082

Qy 772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT---- 819
 | : : : : | : | | : | | : : | : :
 Db 2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142

Qy 820 GSNAVNVFLGIGLAWSVAAIYW 841
 | | | || : | : :
 Db 2143 GENGVR---GIAVDWVAGNLYF 2161

RESULT 7

US-08-652-877-88

; Sequence 88, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjaln, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Savitzky, Martin
 ; REGISTRATION NUMBER: 29,699
 ; REFERENCE/DOCKET NUMBER: A1355E-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-454-3816
 ; TELEFAX: 610-454-3808
 ; INFORMATION FOR SEQ ID NO: 88:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4655 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-652-877-88

Query Match 2.7%; Score 128.5; DB 3; Length 4655;
 Best Local Similarity 18.4%; Pred. No. 0.087;
 Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;

Qy 156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRGIKHL----- 200
 | |:: | : | :: :: :: : | | | :: ::
 Db 1415 CDTGYMLES DGRTCKV-TASESLLLLVSQNKIIADSVTSQVHNIYSLVENGSIYIVAVDF 1473
 Qy 201 -----RVFFITA----AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVA 251
 |:: | || | : || :: : : ||
 Db 1474 DSISGRIFWSDATQGKTWSAFQNGTDRRV--VFDSSII-----LTETIAIDWVG 1520
 Qy 252 DKRLLFYKYMHKKYRTDK---HRGIIIE TEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
 : | : | : | || :: | :::: : | : || | | :
 Db 1521 -RNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSDWGHHPR 1578
 Qy 304 LEGKEVDESREMI-----RIL-----K 321
 : | : | | | : | : |
 Db 1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMDFCDYNGHHRQVIAS 1638
 Qy 322 DLKQKHPEKDLQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS 381
 || : || ||: : | :: : ||: | | | :
 Db 1639 DLIIRHP-----YALTLFEDS-VYWTD RATRRVMRAN---KWHGGNQSVVMY 1681
 Qy 382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-----LENC- 411
 :: | | : : :: | ||: | | ||
 Db 1682 NIQWPLGIVAVHPSKQPN SVNPCAFSRCSHLCLLSSQGPHFYSCVCPSGWSLSPDLLNCL 1741
 Qy 412 --GAVLLTVVRKGGDMSKTMVVDYKTED-----GSANAGADYEFTEGTV----VLKPGE 459
 | ||: : : | : | | | | : | ||
 Db 1742 RDDQPFLITVRQHIIIFGISLNPEVKSNDAMVPIAGIQN-GLDVEFD DAEQYIYWVENPGE 1800
 Qy 460 TQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL--PRAVLASPC 517
 : : | : | : : | ||
 Db 1801 IHR-----VKT DGTNRTVFASISMGVPSMNLA--- 1827
 Qy 518 VATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLR TSG---ARGTVIVPFRTVEGTAK 574
 || : : | : : || | | : | : ||
 Db 1828 -----LDWISRNLY-----STNPRTQSIEVLT LHGDIRYKRLIAN----DGTAL 1868

Qy 575 GGGEDF----EDTYGELEFKNDETVKTIRVKIVDEE-----EY 608
 | | : | : : | : | :
 Db 1869 GVGFPITVDPARGKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTGNLEHLECVTLDI 1928

Qy 609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIIES 667
 | | : : | : | | | : : : | : | : |
 Db 1929 EEQKLYWAVTGRGV-IERGNVDGTD RMIL-----VHQLSHPWGIAVHDSFLYYTDEQ 1979

Qy 668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDESGEERLPSCFDYV 725
 | | | | : | | : : | : | : | : :
 Db 1980 YEVIERVDKATGANKIVL-----RDNVPNLRGLQVYHRRNAAESSNG-----CSNNM 2026

Qy 726 MHFLT VFWKV---LFACV-----PPTYCHGWACFAVSILIIGMLTAIIG---DLAS 771
 : | | : | | : | : : | | : | : :
 Db 2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLSAIRGFSLELSD 2082

Qy 772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT---- 819
 | : : : : | | : | : | : : | : : :
 Db 2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142

Qy 820 GSNVAVNVFLGIGLAWSVAAIYW 841
 | | | | : | : :
 Db 2143 GENGVR--GIAVDWVAGNLYF 2161

RESULT 8

US-08-652-877-90

; Sequence 90, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalm, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:


```

; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4655 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-877-90

```

```

Query Match          2.7%; Score 128.5; DB3; Length 4655;
Best Local Similarity 18.4%; Pred. No. 0.087;
Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;

```

```

Qy      156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKL----- 200
      | |:: | : | :|: :: :: : | | | :: ::
Db      1415 CDTGYMLES DGRTCKV-TASESLLLLVASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDF 1473

Qy      201 -----RVFFITA----AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVA 251
      |::: | | | : | | :: : : : | |
Db      1474 DSISGRIFWSDATQGKTWSAFQNGTDRRV--VFDSSII-----LTETIAIDWVG 1520

Qy      252 DKRLLFYKYMHKKYRTDK----HRGIIIETEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
      : | : | : | | | :: | :|: :| : | | | | :
Db      1521 -RNLWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSDWGHHPR 1578

Qy      304 LEGKEVDESRRMI-----RIL-----K 321
      : | : | | | : | | : |
Db      1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMDFCDYNGHHRQVIAS 1638

Qy      322 DLKQKHPEKDLQLVEMANYYALSHQOKSRAFYRIQATRMGTGAGNILKKHAAEQAKKAS 381
      || :|| |:: : | :: :|| : | | | :
Db      1639 DLIIRHP-----YALTLEFEDS-VYWTD RATRRVMRAN---KWHGGNQSVVMY 1681

Qy      382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-----LENC- 411
      :: | | : : :: | ||: | | |
Db      1682 NIQWPLGIVAVHPSKQPNVNPFCASFRCSHLCLLSSQGPHFYSCVCPSGWSLSPDLLNCL 1741

Qy      412 --GAVLLTVVRKGGDMSKTMVVDYKTED-----GSANAGADYEFTEGTV----VLKPGE 459
      | ||: :: : | : | | | | | : | ||
Db      1742 RDDQPFLITVRQHIIFGISLNPEVKSN DAMVPIAGIQN-GLDVEFD DAEQYIYWVENPGE 1800

Qy      460 TQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL--PRAVLASPC 517
      : : | : | : | |

```

Db 1801 IHR-----VKT DGTNRTVFASISMVGPSMNL A--- 1827

Qy 518 VATVTILDDDHAGIFTFEC DTIHVSE SIGVMEVKVLR TSG---ARGTVIVPFRTVEGTAK 574
 || :: | : ::|| | | :||

Db 1828 -----LDWISRNLY-----STNPRTQSI EVLTLHGDIRYRKT LIAN----DGTAL 1868

Qy 575 GGGEDF----EDTYGELEFKNDET VKTIRVKIVDEE-----EY 608
 | | : | : : | : || :

Db 1869 GVGFPIGITVDPARGKLYWSDQGTDSGVPKIASANMDGTSVKTLFTGNLEHLEC VTLDI 1928

Qy 609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES 667
 | | : : | : || | || : : : | : | :

Db 1929 EEQKLYWAVTGRGV-IERGNVDGTD RMIL-----VHQLSHPWGIAVHDSFLYYTDEQ 1979

Qy 668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDES GEERLPSCFDYV 725
 || || : | || : : | : | : | : :

Db 1980 YEVI ERVDKATGANKIVL-----RDNV PNL RGLQVYHRRNAAESSNG-----CSNM 2026

Qy 726 MHFLT VFWKV---LFACV-----PPTEYCHGWACFAVSILIIGMLTAIIG---DLAS 771
 : | ||: | | : | : : ||: || | : :

Db 2027 NACQQICLPVPGGLFSCACATGFKLNP DN RSCSPYNSF----IVVSMLS AIRGFSLELSD 2082

Qy 772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT---- 819
 | : : : : | | : | : | : : | : : :

Db 2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142

Qy 820 GSNVAVNVLGIGLAWSVAAIYW 841
 | | | || : | : :

Db 2143 GENGVR---GIAVDWVAGNLYF 2161

RESULT 9

US-09-489-039A-13618

; Sequence 13618, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 13618

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13618

Query Match 2.5%; Score 121; DB 4; Length 325;

Best Local Similarity 28.9%; Pred. No. 0.0045;

Matches 46; Conservative 24; Mismatches 59; Indels 30; Gaps 7;

Qy 754 VSILIIGMLTAIIGD----LASHFG---CTIGLKDSVTAVVFVAFGTSVPDTFASKAAAL 806

```

      |::: | | : | |:: | |:: | | |:: | : |
Db      181 VAMIVMPMATRMVVDNSTVLANYFAISELTVGL-----TVVAIGTSLPE-LATAIAGA 232

Qy      807 QDVIYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFT--I 864
      : | |:: |:: |:: |:: |:: |:: | | | : | | |
Db      233 RKGEDDIAIGNIIGANILNIALVLGLPALIAP-----GSFATEAFTRDYGVMLLVSLI 285

Qy      865 FAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
      | | : | | | | | | | | : |
Db      286 FAVLC-----WRRQQQPGRLVGLLVGGFVWVLAMLFW 318

```

RESULT 10

```

US-09-543-681A-5929
; Sequence 5929, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS
MIRABILIS FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5929
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5929

```

```

Query Match          2.4%; Score 116; DB 4; Length 355;
Best Local Similarity 25.1%; Pred. No. 0.016;
Matches 45; Conservative 30; Mismatches 70; Indels 34; Gaps 8;

```

```

Qy      745 YCHGW----ACFAVSILIIGMLTAIIGD-----LASHFGCTIGLKDSVTAVVFVAFGTSV 795
      : | | |:: |:: |:: |:: |:: | | | : | : | | |::
Db      21 FTHCWKTDGMLITLSLLIVGLMLLVYASDRLVYGASVFAQSLKLPPAVIGIVIVGMGTSL 80

Qy      796 PDTFASKAAALQDVIYADASIGNVTGSNAVNVFL--GIGLAWSVAAIYWALQGQEFHVSAG 853
      | : | : |:: :: : : | | |:: | : | | | | | | : :
Db      81 PELFVATDAAIHNL-PEIAIGTAIGSSLTNLLLIAGIG-----AMIY-----PMNIQSA 128

Qy      854 TLAFSVTLFTTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATL 912
      | : | | |:: |:: |:: |:: |:: | | | | : | ::: |
Db      129 VLKKELPLMII-----VILLAGLVVSNHGLGREGCLL----FFIGFASLFLMIKML 176

```

RESULT 11

```

US-08-973-462-8
; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE

```

```
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-08-973-462-8
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Query Match          2.4%; Score 115.5; DB 3; Length 1786;
Best Local Similarity 20.5%; Pred. No. 0.31;
Matches 94; Conservative 79; Mismatches 168; Indels 117; Gaps 22;
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```
Qy      268 DKHRGIIIE--TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQ 325
      :|  :::|  :|  :|  |::  ::  |:  :  |::  ::|  ::|  :
Db      1197 EKDVSLVVEEVQDNDMDSEVE---KVLELKNMEEELMK-DAVEINDITSKLIETQELNE 1252

Qy      326 KHPE--KDLDQLVEMANYYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSM 383
      :  |:::|  |:  |||  |  ::  :  |:|  |:  ::
Db      1253 VEADLIKMEKLKELEK--ALSEDSK-----EIIDAKDDTLEKVIEEHDITTTTL 1300

Qy      384 SEV--HTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSAN 441
      ||  |  ||  ||  |::  :|  |:  ::  :  :  ||
Db      1301 DEVVELKDVEEDKIEKV-----SDLKDLEEDILKEVKEIKELESEILEDYKE----- 1347

Qy      442 AGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPA 501
      ||  ||  |::  |  :||  :  |||  |
Db      1348 -----LKTIEDT-----ILEEKKEIEKDHF-----EKFEEEAEE----- 1376

Qy      502 IFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGT 561
      :  |  |  |  |  ::  |  :  ||  |:
Db      1377 -----IKDLEADILK-EVSSLEVEEEKKLEEVHELKEEVEH-- 1411

Qy      562 VIVPFRTVEGTAKGGGEDFEDTYGEL--EFKNDETVKTIRVKIVDEEEYERQENFFIALG 619
      :|  ::|  :  |:  :|  |  :  ||  ::  |  :  |  |:  ||
Db      1412 IISGDAHIKGLEEDDLEEVDDLKGSILDMLKGD-----MELGDMDK-ESLEDVTTKLG 1463

Qy      620 EPKWMERGISDVTDRLKLTMEEEEEAKRIAEMGKPVLGHPKL-EVIIIEESYEFKTTVDKLI 678
      |  :  ||  |  |:  |:  :  :  :  ||  |:::|  |  |  |
Db      1464 E---RVESLKDVLSSALGMDEEQMKTRKK-----AQRPKLEEVLLKE--EVKEEPKKKI 1512

Qy      679 KKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE 716
      |  :  :  :  |:  :|  ||  :|  ||
Db      1513 TKKKVRFDIKDKEPKDEIVEV----EMKDEDIEEDVEE 1546
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RESULT 12
US-07-853-913-2
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```

; Sequence 2, Application US/07853913
; Patent No. 5338839
; GENERAL INFORMATION:
; APPLICANT: McKay, Ronald D.G.
; APPLICANT: Lendahl, Urban
; TITLE OF INVENTION: Nestin Expression As An Indicator of
; TITLE OF INVENTION: Neuroepithelial Tumors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,913
; FILING DATE: 19920319
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/660,412
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,803
; FILING DATE: 25-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,762
; FILING DATE: 02-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/180,548
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4641AAAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-853-913-2

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Query Match          2.4%; Score 115.5; DB 1; Length 1805;
Best Local Similarity 18.8%; Pred. No. 0.32;
Matches 99; Conservative 89; Mismatches 215; Indels 123; Gaps 18;

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```

Qy      268 DKHRGIIIEGEGDHPKGI-EMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK 326
        |: | :| | | | :|: | :| :| | || | :|:
Db      734 DQEAGRSLQKENQEPLGYEEAEDQMLE-----RLIEKESQESLKSPEENQRIGKPLERE 787

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Query Match 2.4%; Score 113.5; DB 4; Length 339;
 Best Local Similarity 20.4%; Pred. No. 0.026;
 Matches 69; Conservative 53; Mismatches 149; Indels 67; Gaps 12;

```

Qy      195 RKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKR 254
      ||| : | : : | | : : | | : | : | : | : | : | : |
Db      3 RKIKRSDLMF-SIGFIIIAVIIIVALLILFSFVPVGLWISALAA---GVHVGIGTLVGMR 58

Qy      255 LLFYKYMHHKYRTDKHRGIIIIETEGDHPKGIEMDGKMMNSHFL-----DGNL---- 301
      | : | : | : | : | : | : | : | : | : | : | : |
Db      59 L-----RRVSPRKVIAPLIKAHKAGLNLTNNQLESHYLAGGNVDRVVDANIAAQR 108

Qy      302 ----VPLE-GKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQOKSRAFYRI 356
      : | | : | : | : : : : : : : : : : : : : :
Db      109 ADIDLPFERGAIDLGRDVLAVQ--MSVNPVKVIETPFIAGVAMNGIEVKAKARITVRA 166

Qy      357 QATRMMTGAG-NILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL 415
      | : | | : | : | : | : | : | : | : | : | :
Db      167 NIARLVGGAGEETIIARVGEIVSTIGSSEHHT-----EVLENPDNIS 209

Qy      416 LTVVRKG---GDMSKTMVVDYKTEDGSANAGADYE----FTEGTVVLKPGETQKEFSVGI 468
      || : || : : : : | | | | : : : : : : : : :
Db      210 KTVLSKGLDSGTAFEILSIDIADVDISKNIGADLQTEQALADKNIAQAKAEERRAMAVA- 268

Qy      469 IDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
      : : | : : | : : | : | : : |
Db      269 -----SEQEMKARVQEMRAKVVEAESEVPLAMAEAL 299

```

RESULT 14

US-09-134-001C-3350
 ; Sequence 3350, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3350
 ; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3350

Query Match 2.3%; Score 111; DB 4; Length 660;
 Best Local Similarity 19.1%; Pred. No. 0.15;
 Matches 83; Conservative 67; Mismatches 131; Indels 154; Gaps 20;

```

Qy      556 SGARGTVIVPFRTVEG-----TAKGGGEDFE-----DTYGE 586

```

Db	30	STVAGDVIARYKRMQGYDVRILTGTDEHGQKIQEKAQKAGKTELEYLDEMISGIKNLWSK	89
Qy	587	LEFKNDETVKTI--RVKIVDEEEYER-QENFFIALGEPKWMERGISDVTDRKLTMEEEEA	643
Db	90	LEISNDDFIRTTEERHKQVVEKVFERLLKQGDIYLGE---YEGWYSVPDETYTSQLV	145
Qy	644	KRIAEMGKPVLGHP---KLEVIIIEESYEFKTT--VDKLIK-----	679
Db	146	DPVYENGKIVGGKSPDSGHEVELVKEESYFFNINKYTDRLLEFYDENPDFIQPPSRKNEM	205
Qy	680	-----KTNLALVVGTHSWRDQ-----FMEAIT--VSAAGDEDEDES-----	713
Db	206	INNFIKPGLEDLAVSRTSFDWGVVRVPSNPKHVYVWIDALVNYISSLGYLSDDETFLFNKY	265
Qy	714	-----GEERLPSCFDYVMHFLTVMFWKVLFAC---VPPTEYCHGWACFAVSILIIGM	761
Db	266	WPADIHLMKE-----IVRFHSIIWPILLMALDLPLPKKVFAGHWI-----LMKDGK	312
Qy	762	LTAIIGD-----LASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI	815
Db	313	MSKSKGNVVDPNVLIDRYGLDATRYYLMRELPGSDGVFTPEAFVER-----TNYDL	364
Qy	816	GNVTGSNAVNVFLGIGLAWSVAAIYW-----ALQG-----QEFHVSAG	853
Db	365	ANDLG-NLVNRTI-----SMINKYFHGELPAYQGPKHELDEKMEAMALETVKSFNDNME	417
Qy	854	TLAFSVTLFTIFAFV	868
Db	418	SLQFSVALSTVWKFI	432

RESULT 15

US-09-134-001C-3159
; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159

Query Match 2.3%; Score 111; DB 4; Length 10182;
Best Local Similarity 21.2%; Pred. No. 18;

Matches 97; Conservative 70; Mismatches 168; Indels 122; Gaps 22;

```
Qy      310 DESRREMIRILKDLKQ---KHPEKD-----LDQLVEMANYYA-----LSHQOK 349
      | :  ::  || |  :| |  :|| || | :  ||::|
Db      9479 DATSNDLVNQAKDEGQSAIEHHADELPAKLDANQMIDQKVEDINHLISQNPNSNEEK 9538

Qy      350 SRAFYRIQATRMMTGAGN----ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSY 405
      ::  :|  :: | |  : | | |  : : ||  : | :|  :
Db      9539 NKLISQI--NKLVNGIKNEIQQAINKQQIENA--TTKLDEVIETTKKLIIAKAE----AK 9590

Qy      406 QCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFS 465
      | ::  :  | :  |  | :| || : ||  |  | |
Db      9591 QMIKELSQKKRDAINNNTDL-----TPSQKAHALADIDKTE-----KDALQHIENS 9636

Qy      466 VGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFN--SLPLPRAVLASPCVA---- 519
      | |||  || | |:: | :  :  | :|  | | |:: | |
Db      9637 NSI--DDINNNKEHAFNTLAHIIIWDTDQQ----PLVFEVPELSLQNALVTSEVVHRDE 9690

Qy      520 -----TVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
      :| : | :  | :  | : :  :|| : | : || | : ||
Db      9691 TISLESIKKKMTLTDELKVNIVSLP-NTDKVADHL-TAKVKVILADGSYVTNVVPVKVVE 9748

Qy      571 GTAKGGGEDFEDTYGELEFKNDETVKTI-----RVKIVD-----EEEYERQ 611
      || :  : :||  : :| :|  : | ||
Db      9749 -----KELQIAKKDAIKTIDVLVKQIKDIDSNNELTSTQREDAKAEIERL 9794

Qy      612 ENFFIALGEPKWMERGISDVTDRKLTMEEE-----EAKR--IAEMGKPVLGHEH 657
      :  |  :  : | | :  | | ||  :|| : | : :
Db      9795 KKQAI---DKVNHSKSIKDIETVKRTDFEEIDQFDPKRFTLNKAKKDIITDVNTQIQNGF 9851

Qy      658 PKLEVIIIEESYEFKTTVDK---LIKKTNLALVVGTHS 691
      : :| |  :  || ||  : :| | | | :
Db      9852 KEIETIKGLTSNEKTQFDKQLTALQKEFLEKVEHAHN 9888
```

Search completed: June 24, 2004, 16:15:52
Job time : 26.3089 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:07:32 ; Search time 20.9182 Seconds
(without alignments)
4235.175 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	3447.5	71.9	970	2	A36417	Na+/Ca2+-exchangin	
2	3441	71.7	935	2	S43730	Na+/Ca2+-exchangin	
3	3439.5	71.7	973	2	S32815	Na+/Ca2+-exchangin	
4	3437.5	71.7	941	2	B53335	Na+/Ca2+-exchangin	
5	3434.5	71.6	958	2	S32435	Na+/Ca2+-exchangin	
6	3432.5	71.6	970	2	I48097	Na+/Ca2+-exchangin	
7	3426	71.4	957	2	A53789	Na+/Ca2+-exchangin	
8	3425.5	71.4	970	2	S27114	Na+/Ca2+-exchangin	
9	3422	71.3	971	2	S28833	Na+/Ca2+-exchangin	
10	3357	70.0	921	2	A54139	Na+/Ca2+-exchangin	
11	2007	41.8	890	2	B89047	protein C10G8.5 [i	
12	1192	24.8	807	2	T24110	hypothetical prote	
13	659	13.7	152	2	I52640	cardiac sodium/cal	

14	573.5	12.0	538	2	T00424	probable Na ⁺ /Ca ²⁺
15	573	11.9	133	2	A48852	Na ⁺ /Ca ²⁺ -exchangin
16	312	6.5	1199	2	S20969	Na ⁺ /Ca ²⁺ ,K ⁺ -exchan
17	284.5	5.9	1014	2	T31433	Na ⁺ /Ca ²⁺ ,K ⁺ -exchan
18	225	4.7	123	2	I46959	Na/Ca exchanger NA
19	215.5	4.5	591	2	T19746	hypothetical prote
20	205.5	4.3	1568	2	T08616	aggregation factor
21	201	4.2	4936	2	AH2515	hypothetical prote
22	190.5	4.0	2205	2	T08615	aggregation factor
23	170.5	3.6	611	2	T21747	hypothetical prote
24	169.5	3.5	3016	2	S77300	hypothetical prote
25	161	3.4	825	2	T08617	aggregation factor
26	150.5	3.1	591	2	S40705	Na ⁺ /Ca ²⁺ ,K ⁺ -exchan
27	147	3.1	590	2	S40707	hypothetical prote
28	144.5	3.0	703	2	T03888	Na ⁺ /Ca ²⁺ ,K ⁺ -exchan
29	144	3.0	644	2	B96582	hypothetical prote
30	144	3.0	1428	2	AC2224	hypothetical prote
31	143.5	3.0	325	2	F65110	hypothetical 34.7
32	143	3.0	123	2	A53335	Na ⁺ /Ca ²⁺ -exchangin
33	142.5	3.0	325	2	C91138	hypothetical prote
34	142.5	3.0	325	2	F85983	hypothetical prote
35	142.5	3.0	1807	2	JC6319	integrin beta-4 ch
36	142	3.0	302	2	C64311	Na ⁺ /Ca ²⁺ -exchangin
37	141.5	2.9	318	2	G84196	cation antiporter
38	139.5	2.9	826	2	AB1841	hypothetical prote
39	139.5	2.9	1748	1	JN0786	integrin beta-4 ch
40	138	2.9	743	2	T38674	probable membrane
41	135.5	2.8	325	2	AI0904	probable membrane
42	134	2.8	433	2	S74922	hypothetical prote
43	132	2.8	720	2	T02457	hypothetical prote
44	129.5	2.7	309	2	B72342	conserved hypothet
45	128.5	2.7	664	2	S66067	methionine-tRNA li

ALIGNMENTS

RESULT 1

A36417

Na⁺/Ca²⁺-exchanging protein - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000

C;Accession: A36417

R;Nicoll, D.A.; Longoni, S.; Philipson, K.D.

Science 250, 562-565, 1990

A;Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na⁽⁺⁾-Ca⁽²⁺⁾ exchanger.

A;Reference number: A36417; MUID:91047958; PMID:1700476

A;Accession: A36417

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-970 <NIC>

A;Cross-references: GB:M57523; NID:g164072; PIDN:AAA62766.1; PID:g164073; GB:M36119

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

C;Keywords: phosphoprotein; transmembrane protein

Query Match 71.9%; Score 3447.5; DB 2; Length 970;
 Best Local Similarity 69.2%; Pred. No. 1e-223;
 Matches 677; Conservative 109; Mismatches 127; Indels 65; Gaps 10;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : :	
Db	1	MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGERNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIKKPN	118
		: : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFRMSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNM	178
		: : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: : : :	
Db	177	FIIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : :	
Db	237	FFFPICVVFVAVADRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
		: : : : :	
Db	297	VDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYYQC	407
		: : : : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTVAENDPVSKIFFEQGTYYQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : : : : :	
Db	416	LENCGTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFVKPGETQKEIRVG	475
Qy	468	IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
		: : : :	
Db	476	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
		: : : :	
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qy	588	EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG-----	627
		: : : : : : : :	
Db	593	EFQNDIVKTISVKVIDDEEYKNTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHEHPKLEVI	663
		: : : :	
Db	653	YGQPVFRKVHAREHPIPTVITIAEEYDDKQPLTSKEEEEERRIAEMGRPILGEHTKLEVI	712
Qy	664	IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD	723
		: : : : :	
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTHSWREQFIEAITVSAGEDDDDDDECGEELPSCFD	772
Qy	724	YVMHFLTVMFKVLFACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSV	783

Qy 293 NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQVEMANYYALS 345
 ||| ||| || || | | | :||| ||||:|||||:|::||:|:| ||
 Db 294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy 346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
 |||||:|||||:|||||:|||||:|||||:|||||: |||: | | | :|||: :
 Db 353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy 405 YQCLENCGAVLLTVVRKGGDSMTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
 ||||| | | |:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 413 YQCLENCGTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy 465 SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPR-AVLASPCVATVTI 523
 |||||:| | |||: | |:| | : | | | |:|
 Db 473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
 ||||| |||||:||||| |||:|:|:|:|:|:|:|:|
 Db 529 FDDDHAGIFTFEFPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGGEDFEDT 588

Qy 584 YGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWME----RGISDVTD-----R 634
 ||||:| | ||| |:|:|:|:| : | | :|:|: | :| :|: :
 Db 589 CGELEFQND EIVKTISVKVIDDEEYKNTFFIEIGEPRLVEMSEKKGFTLT EYDDKQ 648

Qy 635 KLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRD 694
 || :||| :|||:|:| | |||||:|||||:|||||:|:|:|:|:|:|:|:|
 Db 649 PLTSKEEEERRIAEMGRPILGEHTKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHNSWRE 708

Qy 695 QFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWKVLFAFVPPT EYCHGWACFAV 754
 |:|:| | |:|:| | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 709 QFIEAITVSAGEDDDDDDECGEELPSCFDYVMHFLT VFWKVLFAFVPPT EYWNGWACFIV 768

Qy 755 SILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADAS 814
 |:|:|:| | |||||:|||||:|||||:|||||:| | | |||||
 Db 769 SILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADAS 828

Qy 815 IGNVTGSNAVN VFLGIGLAWSVA AIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLL 874
 |||||:|||||:|:|:| | |:| | | |||||:|:|:|:|:|:|:|:|:|
 Db 829 IGNVTGSNAVN VFLGIGVAWSIA AIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVL 888

Qy 875 YRRRPHLGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||| :||| || | : || | |||| |:|:|:|:|:|
 Db 889 YRRRPEIGELGGPR TAKLLTSSLFVLLWLLYIFFSSLEAYCHIKGF 935

RESULT 3

S32815

Na⁺/Ca²⁺-exchanging protein - human

N;Alternate names: Na⁺/Ca²⁺ antiporter; Na⁺/Ca²⁺ exchanger

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C;Accession: S32815; A56767

R;Komuro, I.; Wenninger, K.E.; Philipson, K.D.; Izumo, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992

A;Title: Molecular cloning and chracterization of the human cardiac Na⁽⁺⁾/Ca⁽²⁺⁾ exchanger cDNA.

C;Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Matches 674; Conservative 111; Mismatches 128; Indels 65; Gaps 10;

Db 4 MRRLSLSP TFSMGEHLLVTVSLLFSHVDHVIAETEME GEGNETGE----CTGSYYCKKGV 59

Db 60 ILPIWEPDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSOEKEITIKKPN 119

Db 120 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAEFNM 179

Db 180 FIIIALCVYVVPDGETR KIKHLRVFEVTAAWSIFAYTWLYIIISVISPGVVEVWEG LITE 239

Db 240 FFFPICVVF~~AW~~ADRLLFYKYVYKRYRAGKORGMII~~IE~~HEGDRPSSKTEIEMDGKVVNSH 299

Db 300 VENFLD GALV-LEVDERDQDDEEARREMARILKELKOKHPDKEIEOLIELANYOVLSOOO 358

Db 359 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTTEVTENDPVSKIFFEOGTYOC 418

Db 419 LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKEPGD~~TOKEIRVG~~ 478

QY 468 I I D D D I F E E D E H F F V R L S N V R I E E E Q P E E G M P P A I F N S L P L P R A V L A S P C V A T V T I L D D D 527

Db 479 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 535

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| :||||| :||| :||| :||| :||| :|||

Db 536 HAGIFTFEFPVTHVSESIGIMEVKVLRITSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 595

Qy 588 EFKNDET VKTIRVKIVDEEYERQENFFIALGEPKWMERG----- 627
 ||: ||| ||| ||: ||: ||| : ||: ||| : ||

Db 596 EFQNDEIVKTISVKVIDDEEYEKNKTFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL 655

Qy 628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVI 663
 |:| | | | :||| :||| :||| :|||

Db 656 FGQPVFRKVVHAREHPILSTVITIAD EYDDKQPLTSKEEEEERRIAEMGRPILGEHTKLEVI 715

Qy 664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD 723
 ||||| :||||| :||| :||: ||||| |:|: ||| :|||

Db 716 IEESYEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDDECGEEKLPSCFD 775

Qy 724 YVMHFLT VFWKVLFAFVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV 783
 ||||| :||| :||| :||: ||| |||||

Db 776 YVMHFLT VFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSV 835

Qy 784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
 ||||| ||||| || || ||||| :||| :||| :||| :|||

Db 836 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 895

Qy 844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
 |:| || ||||| : ||||| :||| || ||| ||

Db 896 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSCFLVLLW 955

Qy 904 LLYILFATLEAYCYIKGF 921
 |||| |:|: ||||: ||||

Db 956 LLYIFFSSLEAYCHIKGF 973

RESULT 4

B53335

Na⁺/Ca²⁺-exchanging protein NCX1, splice form NACA6 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000

C;Accession: B53335

R;Kofuji, P.; Lederer, W.J.; Schulze, D.H.

J. Biol. Chem. 269, 5145-5149, 1994

A;Title: Mutually exclusive and cassette exons underlie alternatively spliced isoforms of the Na/Ca exchanger.

A;Reference number: A53335; MUID: 94148976; PMID: 8106495

A;Accession: B53335

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-941 <KOF>

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:144050)

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 71.7%; Score 3437.5; DB 2; Length 941;

Best Local Similarity 71.0%; Pred. No. 4.7e-223;

Matches 669; Conservative 111; Mismatches 125; Indels 37; Gaps 11;

Qy	8	PLTSAFLHFGLVTFVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE	66
Db	9	PFSMGFHLAIVALFFFRVDHVSAAETEMEGEGETGE---CTGSYYCKKGVILPIWEPQ	64
Qy	67	NPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTI	126
Db	65	DPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKK-NGETTKTTV	123
Qy	127	RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICV	186
Db	124	RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIALCV	183
Qy	187	YVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVL	246
Db	184	YVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV	243
Qy	247	LAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FLDGN	300
Db	244	FAWVADRRLLFYKYVYKRYRAGKQGRMIIIEHGEDRPSSKTEIEMDGKVVNSHVDNFLDGA	303
Qy	301	LVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQVLVEMANYYALSHQQKSRAFYRI	356
Db	304	LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI	362
Qy	357	QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL	415
Db	363	QATRLMTGAGNILKRHAADQARKAVSMHEVNTEMAENDPVSKIFFEQGTQCLENCGTVA	422
Qy	416	LTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE	475
Db	423	LTIIRRGDGLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE	482
Qy	476	EDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFE	535
Db	483	EDENFLVHLNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDHAGIFTFE	539
Qy	536	CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	540	ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFQNDIV	599
Qy	596	KTIRVKIVDEEEYERQENFFIALGEPKWMERG-----ISDVTDRK--LTME	639
Db	600	KTISVKVIDDEEYEKNKTFLEIGEPRLVEMSEKKALLLNELGGFTITEEYDDKQPLTSK	659
Qy	640	EEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEA	699
Db	660	EEEEERIAEMGRPILGEHTKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHNSWREQFIEA	719
Qy	700	ITVSAAGDEDEDESGEERLPSCFDYVMHFLTTFVFKVLFACVPPTTEYCHGWACFAVSILII	759
Db	720	ITVSAGEDDDDDDECGEELPSCFDYVMHFLTTFVFKVLFACVPPTTEYWNGWACFIVSILMI	779
Qy	760	GMLTAIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVT	819
Db	780	GLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTEFASKVAATODOYADASIGNVT	839

```

Qy      820 GSNVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRP 879
      .  |||||:||||| | : | | |||||: : |||||
Db      840 GSNVNVFLGIGVAWSIAAIYHAANGEHFKVSPGTLAFSVTLFTIFAFINVGVLlyRRRP 899

Qy      880 HLGGE LGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
      : ||||| | | : || ||||| | : |||||
Db      900 EIGGE LGGPRTAKLLTSCLEVLWLLYIEFSSLEAYCHIKGF 941

```

S32435

Na⁺/Ca²⁺-exchanging protein RBE-2 - rat

N; Alternate names: Na⁺/Ca²⁺ antiporter; sodium-calcium exchanger RBE-2

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 18-Aug-2000

C;Accession: S32435

R; Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 319, 105-109, 1993

A;Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene and their functional expression in HeLa cells.

A;Reference number: S32435; MUID:93202244; PMID:8454039

A;Accession: S32435

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-958 <FUR>

A;Cross-references: EMBL:X68813; NID:q288231; PIDN:CAA48708.1; PID:q288232

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 71.6%; Score 3434.5; DB 2; Length 958;
Best Local Similarity 69.6%; Pred. No. 7.6e-223;
Matches 675; Conservative 106; Mismatches 124; Indels 65; Gaps 11;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGSGDVPSTGQNNESCSGSSDCK	55
Db	2	LRLSLPPNVSMGFRVLTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKJARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIK	115
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIDRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEG	235
Db	174	FNMFIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEG	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
Db	234	LTLFFFPICVVFVAVADRLLFYKYVYKRYRAGKQRMIIIEHGEDRPASKTEIEMDGKV	293
Qy	293	NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYALS	345
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQOKSRAFYRIQATRMMTGAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-970 <RES>
A;Cross-references: EMBL:U04955; NID:g927230; PIDN:AAA73904.1; PID:g507350
C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 71.6%; Score 3432.5; DB 2; Length 970;
Best Local Similarity 68.7%; Pred. No. 1.1e-222;
Matches 672; Conservative 112; Mismatches 129; Indels 65; Gaps 11;

Qy	1	MAWLRLQPLTSAFLH-FGLVTFVL-FLNGLRAEAGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : :	
Db	1	MLRLSLSPYSLGFHLLAMMTLLISHVDHITAET----EMVEEGNETGECTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
		: : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
		: :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : :	
Db	237	FFFPICVFAWVADRRLLFYKYVYKRYRAGKQRMIIIEHEDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
		: : : : :	
Db	297	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
		: : : : : : : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : : : : : : : : :	
Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKEPGETQKEIRVG	475
Qy	468	IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
		: : : : :	
Db	476	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHIS---TLACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
		: : : :	
Db	533	HAGIFTFEPPVTHVSESIGIMEVKVLRITSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qy	588	EFKNDETVKTIRVKIVDEEYERQENFFIALGEPKWMERG-----	627
		: : : : : : : : : : : :	
Db	593	EFQNDIVKTISVKVIDDEEYKNTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKHL	652
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVI	663
		: : : : : : :	
Db	653	YGQPVLRKVHARDHIPSTVITIADEYDDKQPLTSKEEEERRIAELGRPILGEHTKLEVI	712

Qy 664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD 723
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 713 IEESYEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDDECGEKLPSCFD 772

Qy 724 YVMHFLTVMFKVLFACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSV 783
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 773 YVMHFLTVMFKVLFACVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSV 832

Qy 784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 833 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 892

Qy 844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSLW 903
 |:|:| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLRYRRRPEIGELGGPRTAKLLTSCLFVLLW 952

Qy 904 LLYILFATLEAYCYIKGF 921
 |||| |:|:|:|:|:|:|
 Db 953 LLYIFFSSLEAYCHIKGF 970

RESULT 7

A53789

Na+/Ca2+-exchanging protein precursor, splice form NACA7 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000

C;Accession: A53789; JX0288

R;Lee, S.L.; Yu, A.S.L.; Lytton, J.

J. Biol. Chem. 269, 14849-14852, 1994

A;Title: Tissue-specific expression of Na(+)-Ca(2+) exchanger isoforms.

A;Reference number: A53789; MUID:94253030; PMID:8195112

A;Accession: A53789

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-957 <LEE>

A;Cross-references: GB:U04933; NID:g451571; PIDN:AAB39952.1; PID:g451572

R;Nakasaki, Y.; Iwamoto, T.; Hanada, H.; Imagawa, T.; Shigekawa, M.

J. Biochem. 114, 528-534, 1993

A;Title: Cloning of the rat aortic smooth muscle Na+/Ca2+ exchanger and tissue-specific expression of isoforms.

A;Reference number: JX0288; MUID:94103175; PMID:8276763

A;Accession: JX0288

A;Molecule type: mRNA

A;Residues: 1-957 <NAK>

A;Experimental source: aortic smooth muscle

C;Superfamily: human Na+/Ca2+-exchanging protein

C;Keywords: ion transport; membrane protein

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-957/Product: Na+/Ca2+ exchanger #status predicted <MAT>

Query Match 71.4%; Score 3426; DB 2; Length 957;

Best Local Similarity 69.6%; Pred. No. 2.8e-222;

Matches 674; Conservative 105; Mismatches 126; Indels 64; Gaps 11;

Qy 4 LRLQPLTSAFLHFGVLTVFLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55

||| : : | || | | || ||: ||| ||

Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVITIK	115
Db	54	KGVLPIWEPQDPSFGDKIARATVYFVAMVYMLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
Db	114	KPNGETTKTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
Db	174	FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
Db	234	LTFFFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPAKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLQLVEMANYALS	345
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMGTGAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNIIKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRGGDLTNTVVFDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRSSEVSEDG----ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPIYKTIEGTARGGGEDFEDT	588
Qy	584	YGELEFKNDETVKTIKIVDEEEYERQENFFIALGEPKWMERG-----	627
Db	589	CGELEFQNDIEVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTGQPVFRKV	648
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVIIEESYEFKT	672
Db	649	HARDHPIPSTVISISEEYDDKQPLTSKEEEEERRIAEMGRPILGHTKLEVIIEESYEFKS	708
Qy	673	TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVE	732
Db	709	TVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDCEGEEKLPSCFDYVMHFLTVE	768
Qy	733	WKVLFACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG	792
Db	769	WKVLFVAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALG	828
Qy	793	TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSA	852
Db	829	TSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSP	888

Qy 853 GTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATL 912
 . |||||: : ||||| :||| || |: |||.||| |:|
 Db 889 GTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSL 948
 Qy 913 EAYCYIKGF 921
 |||:||||
 Db 949 EAYCHIKGF 957

RESULT 8

S27114

Na+/Ca2+-exchanging protein precursor, cardiac - bovine

N;Alternate names: Na+/Ca2+ antiporter

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 18-Aug-2000

C;Accession: S27114; S18388

R;Aceto, J.F.; Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson, K.D.; Reeves, J.P.

Arch. Biochem. Biophys. 298, 553-560, 1992

A;Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.

A;Reference number: S27114; MUID:93037494; PMID:1416984

A;Accession: S27114

A;Molecule type: mRNA

A;Residues: 1-970 <ACE>

A;Cross-references: GB:L06438; NID:g163033; PIDN:AAA30509.1; PID:g163034

R;Durkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.

Arch. Biochem. Biophys. 290, 369-375, 1991

A;Title: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium exchanger: evidence for the presence of a signal sequence.

A;Reference number: S18388; MUID:92027750; PMID:1929404

A;Accession: S18388

A;Molecule type: protein

A;Residues: 33-40, 'X', 42-44 <DUR>

A;Experimental source: heart

C;Superfamily: human Na+/Ca2+-exchanging protein

C;Keywords: cardiac muscle; heart; ion transport; membrane protein

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-970/Product: Na+/Ca2+ exchange protein, cardiac #status predicted <MAT>

Query Match 71.4%; Score 3425.5; DB 2; Length 970;

Best Local Similarity 68.7%; Pred. No. 3.1e-222;

Matches 672; Conservative 110; Mismatches 131; Indels 65; Gaps 10;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
 | | | | : :| : : | | : | | :| | :|
 Db 1 MLQFSLSPTLSMGFHVIAVALLFSHVDHISAETEMEGETNETGE---CTGSYYCKKGV 56
 Qy 59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
 |||| |:| | |||| :|||:|||||:|||||:|:||||
 Db 57 ILPIWEPQDPSPFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116
 Qy 119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
 |||: ||:|:|||||:|||||:||||| | |||||
 Db 117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176
 Qy 179 FIIIGICVYVIPDGETRKHHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
 ||| :|||:|||||:||||| |||:|:| ||||:|||||

Db 177 FIIIALCVYVVPDGETRKHILRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF 236

Qy 239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
 ||||:|: ||||:|||||||:|:| | ||:| | | ||||:| |

Db 237 FFFPICVVFVAVDRRLLFYKYVYKRYRAGKQKQGMIIIEHEDRPSKTEIEMDGKVVNSH 296

Qy 296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ 348
 ||| | | | | | :||| |||:|||||||:|:|:| | | |

Db 297 VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy 349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
 |||||:|:|||||||:|:|:| | | | | | :|:|: | |

Db 356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTVAENDPVSKIFFEQGTIYQC 415

Qy 408 LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 |||| | | :|:|:|:|:|:|:|:|:|:|:|:|:|:|:| |

Db 416 LENCCTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | ||||:| | :|:| | | | | | |||| |

Db 476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| | |||||:||||||| ||||:|:|:|:|:|:| |||

Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy 588 EFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERG----- 627
 |:| | | | | :|:|:|:|:| : | | :|:|:|

Db 593 EFQND EIVKTISVKVIDDEEYEKNKTFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL 652

Qy 628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVI 663
 |:| | | | | :| | :|:|:|:|:|:| | | |

Db 653 YGQPVFRKVVHAREHPLPSTIITIAD EYDDKQPLTSKEEEEERRIAEMGRPILGEHTRLEVI 712

Qy 664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD 723
 |||||:|:|||||||:|:|:|:|:|:| | | | | |

Db 713 IEESYEFKSTVDKLIKKTNLALVVGTSNSWREQFIEAITVSAGEDDDDDDECGEELPSCFD 772

Qy 724 YVMHFLT VFWKVLFAFVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSV 783
 ||||| | | | | | :| | | | | :|:|:| | | | | |

Db 773 YVMHFLT VFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV 832

Qy 784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
 ||||| | | | | | | | | | | | | | | | | :|:|:| |

Db 833 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 892

Qy 844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSLW 903
 |:| | | | | | | | | : | | | | | :|:|:| | | |

Db 893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLRYRRRPEIGELGGPRTAKLLTSCLFVLLW 952

Qy 904 LLYILFATLEAYCYIKGF 921
 ||| |:|:|:|:|:|

Db 953 LLYIFFSSLEAYCHIKGF 970

Na⁺/Ca²⁺-exchanging protein - rat
 N;Alternate names: Na⁺/Ca²⁺ antiporter; Na⁺/Ca²⁺ exchanger
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
 C;Accession: S28833; S25552
 R;Low, W.; Kasir, J.; Rahamimoff, H.
 FEBS Lett. 316, 63-67, 1993
 A;Title: Cloning of the rat heart Na(+)-Ca(2+) exchanger and its functional expression in HeLa cells.
 A;Reference number: S28833; MUID:93138118; PMID:8422940
 A;Accession: S28833
 A;Molecule type: mRNA
 A;Residues: 1-971 <LOW>
 A;Cross-references: EMBL:X68191; NID:g57208; PIDN:CAA48273.1; PID:g57209
 R;Low, W.; Kasir, J.; Boulter, J.; Heinemann, S.; Rahamimoff, H.
 submitted to the EMBL Data Library, August 1992
 A;Reference number: S25552
 A;Accession: S25552
 A;Molecule type: mRNA
 A;Residues: 1-194, 'F', 196-971 <LO2>
 A;Cross-references: EMBL:X68191
 C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
 C;Keywords: ion transport; membrane protein; phosphoprotein

Query Match 71.3%; Score 3422; DB 2; Length 971;
 Best Local Similarity 68.6%; Pred. No. 5.4e-222;
 Matches 674; Conservative 106; Mismatches 125; Indels 78; Gaps 11;

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Qy      4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGSGDVPSTGQNNESCSGSSDCK 55
      ||| : : | || | | || ||: |:|| ||
Db      2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy     56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
      :||||| |:| | |||| | ||||:|||||||:|||||:|:|
Db     54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113

Qy    116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAA 175
      ||||| |:|:||||||| |||||:||||| | |||||
Db    114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173

Qy    176 FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
      ||||| :|||:||||||| |||||:||||| |||:|:| ||||:||||
Db    174 FNMFIILALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233

Qy    236 LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMM 292
      || ||||:|: ||| :|||||:|:| | ||:| | || | ||||:
Db    234 LTLFFFPICVFAWVAARRLLFYKYVYKRYRAGKQRMIIIEHGDRPASKTEIEMDGKVV 293

Qy    293 NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYSALS 345
      ||| ||| || | | | :||| |||:|||||:|:|:| || ||
Db    294 NSHVDNFDLGDALV-LEVDERDQDDEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy    346 HQQKSRAFYRIQATRMGTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
      ||||| |||||:|||||||:|:|:| || ||: | | | :|||: :
Db    353 QQQKSRAFYRIQATRLMTGAGNILLKHAADQARKAVSMHEVNMDVVENDAVSKVFFEQGT 412

Qy    405 YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464

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      ||||| | ||::|||: |::||::|||:||||:|||||: |||||
Db      413 YQCLNCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
Qy      465 SVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
      |||||:|||||:| ||||: | |: | : | || ||:|
Db      473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
Qy      524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
      ||||| |||||:||||| ||::||:||||:|||||
Db      529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLR TSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qy      584 YGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMER----- 626
      ||||:||| ||| ||::||:||||: | || :|||: |
Db      589 CGELEFQND EIVKTISVKVIDDEEY EKNKTF FIEIGEPRLVEMSEKKALLLNELGGFTLT 648
Qy      627 -----GISDVTDRK--LTMEEEEAKRIAEMGKPV LGEHP 658
      ||: | | | :||| :|||||:|:||||
Db      649 EGKKMYGQPVFRKVHARDHPI PSTVISISEEYDDKQPLTSKEEEEERRIAEMGRPILGEHT 708
Qy      659 KLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERL 718
      |||||:|||||:||||| ||::||:||||| ||:| | ||:|
Db      709 KLEVIIIEESYEFKSTVDKLIKKTNLALVVG TNSWREQFIEAITVSAGEDDDDDDEC GEEKL 768
Qy      719 PSCFDYVMHFLT VFWKVLFA CVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIG 778
      |||||:|||||:||||| ||||:||||| ||||:|||||
Db      769 PSCFDYVMHFLT VFWKVLFAFVPPT EYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIG 828
Qy      779 LKDSVTAVVFVAFGT SVPDTFASKAAALQDVYADASIGNVTGSNAVN VFLGIGLAWSVAA 838
      ||||| ||||| || || |||||:|||||
Db      829 LKDSVTAVVFVALGT SVPDTFASKVAATQDQYADASIGNVTGSNAVN VFLGIGVAWSIAA 888
Qy      839 IYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWL 898
      || | |:| || |||||: ||||| :||||| || |:|
Db      889 IYHAANGEQFKVSPGTLAFSVTLFTIFAFINVG VLLYRRRPEIGGELGGPRTAKLLTSSL 948
Qy      899 FVSLWLLYILFATLEAYCYIKGF 921
      || ||||| |:| ||||:||||
Db      949 FVLLWLLYIFFSSLEAYCHIKGF 971

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RESULT 10

A54139

Na⁺/Ca²⁺-exchanging protein NCX2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 18-Aug-2000

C;Accession: A54139

R;Li, Z.; Matsuoka, S.; Hryshko, L.V.; Nicoll, D.A.; Bersohn, M.M.; Burke, E.P.;
Lifton, R.P.; Philipson, K.D.

J. Biol. Chem. 269, 17434-17439, 1994

A;Title: Cloning of the NCX2 isoform of the plasma membrane Na⁽⁺⁾-Ca⁽²⁺⁾
exchanger.

A;Reference number: A54139; MUID:94292496; PMID:8021246

A;Accession: A54139

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-921 <LIA>

A;Cross-references: GB:U08141; NID:g511680; PIDN:AAA19920.1; PID:g511681

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
C;Keywords: transmembrane protein

Query Match 70.0%; Score 3357; DB 2; Length 921;
Best Local Similarity 69.6%; Pred. No. 1.2e-217;
Matches 635; Conservative 130; Mismatches 114; Indels 34; Gaps 9;

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Qy      31 EAGGSGDVPSTGQNNE-----SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALI 85
      || : :| | : | || | : ||:|:| | :||| || :|||:|:
Db      21 EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMV 80

Qy      86 YMFLGVSIIDRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA 145
      ||||:|||||:|||||:|:|:| | |||| | :|:|||||:|||||
Db      81 YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA 140

Qy     146 PEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFI 205
      ||||:|||| | | :|| | |||||:|:| :||| | :|||:|:|:
Db     141 PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVVIACVYVIPAGESRKIKHLRVFFV 200

Qy     206 TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
      |:|||||:|:|:|:|:|:|:| | | | ||||: | :|||:|:|:|:|
Db     201 TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFPVCVVFAMADKRLLFYKYVYKRY 260

Qy     266 RTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRIL 320
      ||| ||| ||| || | :|| : : : | | | | :|:| |||:|:|
Db     261 RTDPRSGIIIGAEGDPPKSIELDGTFGTE-VPGELGALGTGPAEARELDASRREVIQIL 319

Qy     321 KDLKQKHPEKDLQQLVEMANYALSHQOKSRAFYRIQATRMGTAGNILKKHAAEQAKKA 380
      |||||:|:|:|:| | :| ||| | |||||:|:|:|:|:|:|:|:|:|:|
Db     320 KDLKQKHPDKDLEQLVGIKYYALLHQOKSRAFYRIQATRLMTAGNVLRRHAADAARRP 379

Qy     381 SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSA 440
      : : : | : :| | :||:| | | ||||:|:|:| :|: : | |||:|:|
Db     380 GA-NDGAPDDEDDGASRIFFEPSLYHCLENC SVLLSVACQGGEGNSTFYVDYRTEDGSA 438

Qy     441 NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQ----PEE 496
      ||:|:|:|:|:| | ||||| :|||:|:|:|:|:|:|:|:|:|:|:|:|
Db     439 KAGSDYEYSEGLTVFKPGETQKELRIGIIDDDIFEDEHFFVRLNLRVGDAQGMFEPDG 498

Qy     497 GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTS 556
      | | : | :| :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     499 G-----GRPKGRLVAPLLATVTILDDDHAGIFSQDRLLHVSECMGTVDVRVVRSS 549

Qy     557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEYERQENFFI 616
      ||||| :|:|:|:|:|:| | :|| |||| :|:|:|:|:|:|:|:|:|:|
Db     550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETMKTLQVKIVDEEYKKNFFI 609

Qy     617 ALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVLGEPKLEVIIIEESYEF 670
      ||:|:|:|:| | : |||| | ||||:|:|:|:|:|:|:|:|:|:|
Db     610 ELGQPQWLKRGISALLLNQGDGRKLTAEEEEAQRIAEMGKPVLGENCRLVIIIEESYDF 669

Qy     671 KTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHF 728
      | |||||:|:|:|:|:|:| | | | ||||:|:| | | |||||:|:|
Db     670 KNTVDKLIKKTNLALVIGTHSWREQFLEAVTVS-AGDEEDEDGSRERLPSCFDYVMHF 728

Qy     729 LTVFWKVLFACVPPTHEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788
      |||||:|:|:|:|:| | | | :|:|:|:|:|:|:|:|:|:| | | |
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Db 729 LTVFWKVLFACLPPEYCHGWACFGVCILVIGLLTALIGDLASHFGCTVGLKDSVNAVVF 788

Qy 789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAYWALQGQEF 848
 || |||:||||| |||| | |||||:|||||:|:|:|:|:|:|

Db 789 VALGTSIPDTFASKVAALQDQCADASIGNVTGSNAVNVFLGLGVAWSVAAYWAVQGRPF 848

Qy 849 HVSAGTLAFSVTLFTTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYIL 908
 | |||||:|||| |:| |||||:| ||||| ||| ||: || ||||

Db 849 EVRTGTALAFSVTLFTVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWFLYIL 908

Qy 909 FATLEAYCYIKGF 921
 ||:|||||:|:|

Db 909 FASLEAYCHIRGF 921

RESULT 11

B89047

protein C10G8.5 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C;Accession: B89047

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ for a list of authors

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999

A;Accession: B89047

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-890 <STO>

A;Cross-references: GB:chr_V; PIDN:AAB09172.1; PID:g1572830; GSPDB:GN00023;

CESP:C10G8.5

C;Genetics:

A;Gene: C10G8.5

A;Map position: 5

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 41.8%; Score 2007; DB 2; Length 890;

Best Local Similarity 45.9%; Pred. No. 7.7e-127;

Matches 416; Conservative 145; Mismatches 232; Indels 114; Gaps 13;

Qy 87 MFLGVSIIDRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP 146
 ||||:|:|||||:||||| || : |:| : :|:|:|:|:|:|:|

Db 1 MFLGISIVADRFMSSIEVITSMEERTIVVKRPGLDPMVQVRIWNDTVSNLTLMALGSSAP 60

Qy 147 EILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHKLRFVFFIT 206
 ||||:| | |||||:|||||:|:| || || || |: || || :|

Db 61 EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVVVIPKGEIRQKHLDFVFCVT 120

Qy 207 AAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYR 266
 | ||:|:|:|:|:| |||| :|:| || |||:| |:| |:| |:| :|

Db 121 ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFFIFFPLTVFTAYMADIKLIQNKFLPHRYR 180

RESULT 12
T24110
hypothetical protein ZC168.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*

T24110

hypothetical protein ZC168.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T24110; T27507
 R;Berks, M.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z19841
 A;Accession: T24110
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-807 <WIL>
 A;Cross-references: EMBL:Z70309; PIDN:CAA94363.1; GSPDB:GN00022; CESP:ZC168.1
 A;Experimental source: clone R102
 R;Berks, M.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z20378
 A;Accession: T27507
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-807 <WI2>
 A;Cross-references: EMBL:Z70312; PIDN:CAA94387.1; GSPDB:GN00022; CESP:ZC168.1
 A;Experimental source: clone ZC168
 C;Genetics:
 A;Gene: CESP:ZC168.1
 A;Map position: 4
 A;Introns: 38/1; 177/3; 346/1; 365/1; 369/3; 414/3; 455/3; 692/3; 743/2

Query Match 24.8%; Score 1192; DB 2; Length 807;
 Best Local Similarity 33.6%; Pred. No. 4.6e-72;
 Matches 302; Conservative 150; Mismatches 320; Indels 126; Gaps 20;

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Qy      47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
      | | : | | |::: | : | | | | | | | | | | | | | |
Db      2 SSSANLTCKNGILI-----PALETTPRNAILYLAGLFYCFGLGIAIAADIFMCSIEQIT 54

Qy     107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      | : | : | | : | : | | | | | | | | | | | | | | |
Db     55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114

Qy     156 CGHGFIAAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYI 215
      | : | | | | | | | | | | | | | | | | | | | | |
Db     115 VGNGFKAGDLGPGTIVGSAAFNLCISAICVFAV-GTQTKRIELRVFVVTAFFGTAYI 173

Qy     216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTD----- 268
      | : : : | | : | | | | | | | | | | | | | | | |
Db     174 WVFLVLIVITPNVVDVWEAILTLFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy     269 -KHRGIIIEETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRRMIRILKDL 323
      : | | : | | : : | | : : : : | | | | | | : :
Db     229 AQHDGKV----DDQPEKLSDEIKKWASNLNKEENDVIVDATPSVDTVIR----RWTRSI 280

Qy     324 KQKHPEKDLQVLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSM 383
      : | : : : | | : | | | | | : : : : | | : | :
Db     281 SHTYPSLSDEDQAKILAYRVSRTMSHDRLYYRIRAIRQLSSS---WRKSEEEVLKMNQ 337

Qy     384 SEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAG 443
      | | : | | | : | | | | | | | | | | | | | |
Db     338 ES--TDSASRRKTFVEFSARVYRVDATDETVSLKIERK-GNMESKFTVSYATVNLAKKD 394

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Qy      444 ADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIF 503
      :: | | : || | | : :: : | | : ::
Db      395 LNFLFKSETLQFNPGELHKTISIQLINAANWRPNDFVYVHLKIQDVDED----- 443

Qy      504 NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH-VSESIGVMEVKVLRITSG-ARGT 561
      : | : | : || | : | | : | | : | | :
Db      444 -----SKICLGA-----CNVAHVVKENAGFSRSFVTRRGGLKKP 478

Qy      562 VIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEP 621
      : | : | : || | : | | : | | : :: :: : | | | |
Db      479 LQVHYETEDVTAKQGGDYTAVKDGILGFEGQEYEKYIDIDVIDDKMDEKDEAFIIE--L 536

Qy      622 KWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHEHPKLEVIIIEESYEFK--TTVDKLIK 679
      | | | : | | | : | | : | | | :
Db      537 KVDEPGVSIGTRRKATI-----TIISDDNVLKNITNVRKLMG 573

Qy      680 KTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWKVLFAC 739
      | | : :: : | : :: : | : : | : | | |
Db      574 HYMRQLRPGKATWKEQILNAVSVNA-----GDLANATVSDCILHALAFPWKFAFAF 624

Qy      740 VPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTF 799
      : || : | : || : :: || : :: || : :: || : || : || : || : ||
Db      625 LPPPTIFYGYPCFVVALIGIGLVTA VVGDVASIFGCMVGLKDAVTAITLVALGTSLPDTF 684

Qy      800 ASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQQQEFHVSAGTLAFSV 859
      || | || | | : : || || || : || || : : || : : | | | | ||
Db      685 ASKIAAESDDTADNAVGNVTGSNSNVNVLGLGLPWVIASLYWASKGESFRVDAGDLGFSV 744

Qy      860 TLFTIFAFVCISVLLYRRRPHL--GGELGGPRGCKLATTWLFVSLWLLYILFATLEAY 915
      | : | | : : : || : || : || || | | : | | || : : : : |
Db      745 TVFMICSVLFLVLVLRRKLKAFGQGELGGPFGTKLSALFFVGLWIVYVGLSIWKMY 802

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RESULT 13

I52640

cardiac sodium/calcium exchanger, cerebellar granule neurons - rat (fragment)

C;Species: Rattus sp. (rat)

C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Aug-2000

C;Accession: I52640

R;Marlier, L.N.; Zheng, T.; Tang, J.; Grayson, D.R.

Brain Res. Mol. Brain Res. 20, 21-39, 1993

A;Title: Regional distribution in the rat central nervous system of a mRNA encoding a portion of the cardiac sodium/calcium exchanger isolated from cerebellar granule neurons.

A;Reference number: I52640; MUID:94077033; PMID:8255180

A;Accession: I52640

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-152 <RES>

A;Cross-references: GB:S67769; NID:g459304

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

C;Keywords: cardiac muscle; heart

Query Match 13.7%; Score 659; DB 2; Length 152;

Best Local Similarity 82.9%; Pred. No. 3.2e-37;

Matches 126; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy	700	ITVSAAGDEDEDESGEERLPSCFDYVMHFLTVMFKVLFACVPPTTEYCHGWACFAVSILII	759
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Db	1	ITVSAGEDDDDDDECGEELPSCFDYVMHFLTVMFKVLFVFPPTTEYWNGWACFIVSILMI	60
Qy	760	GMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVDPDTFASKAAALQDVYADASIGNVT	819
		:	
Db	61	GLLTAFIGDLASHFGCTIGLKDSVTAVVFVAFGTSVDPDTFASKVAATQDQYADAFIGNVT	120
Qy	820	GSNAVNVFLGIGLAWSVAAIYWALQGQEFHVS	851
		: :	
Db	121	GSNAVNVFLGIGVAWSIAAIYHAANGEOKVS	152

Db	29	FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTTIDPITKAEV	87
Qy	124	TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF	179
Db	88	ITYKKVWNFTIADISLLAFGTSFPQISLATIDAIRNMGERY-AGGLGPGTLVGSAAFDLF	146
Qy	180	IIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF	239
Db	147	PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL	206
Qy	240	FFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDG	299
Db	207	QYGLLLVHAYAQDKR---WPYLS-----LPMSRGDRPE-----	236
Qy	300	NLVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVLVEMANYYALSHQKSRIFYRIQAT	359
Db	237	EWVP---EEIDTSK-----DDNDND-----	253
Qy	360	RMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVV	419
Db	254	-----VHDVYSDAQAQDAV-----	266
Qy	420	RKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEH	479
Db	267	-----ESGSRN-----IVD-----	275
Qy	480	FFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTI	539
Db	276	-----IF-----SI	279
Qy	540	HVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIR	599
Db	280	H-----SANNDTGITYHTVADTPP-----DSATKKGK	306
Qy	600	VKIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHEPK	659
Db	307	AK-----	308
Qy	660	LEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLP	719
Db	309	-----NSTVFDI-----WKHQFVDAITVKIF-----NLP	332
Qy	720	SCFDYV-----MHFLTTFWVKVLFACVPPTTEYCHGWACFAVSILIIGMLTAIIGDLASHF	773
Db	333	MDSIYLRIAKSFWHLLLAPWKLLFAFVPPCNIAHGWI AFICSLLFISGVAFVVTRFTDLI	392
Qy	774	GCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLA	833
Db	393	SCVTGINPYVIAFTALASGTSWPDLVASKIAAERQLTADSAIANITCSNSVNIYVGIGVP	452
Qy	834	WSVAAI--YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGC	891
Db	453	WLINTVYNYFAYREPLYIENAKGLSFSLLIFFATSVGCIVVLVLRRL-IIGAELGGPRLW	511
Qy	892	KLATTWLFVSLWLLYILFATLE	913

512 AWLTSAYFMMLWVVFVVI.SSLK 533

A48852

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A48852

Am. J. Physiol. 263, F680-F685, 1992

A;Reference number: A48852; MUID:93035974; PMID:1415740

A;Accession: A48852

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-133 <YU1>

A;Experimental source: kidney

A;Note: sequence extracted from NCBI backbone (NCBIP:116872)

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 11.9%; Score 573; DB 2; Length 133;

Best Local Similarity 84.2%; Pred. No. 1.6e-31;

Matches 112; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 730 TVFWKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFFV 789
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Db 1 TVFWKVL FANVP PTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVV FV 60

Qy 790 AFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFH 849
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Db 61 ALGTSVPDTFASKVAATQDQYRDASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGE OFK 120

Qy 850 VSAGTLAFSVTLF 862
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Db 121 VSPGTLAFSVTLF 133

Search completed: June 24, 2004, 16:15:01

Job time : 24.9182 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:12:03 ; Search time 50.8014 Seconds
(without alignments)
5118.180 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQLPLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length DB	ID				Description

1	4797	100.0	921	9	US-09-804-474A-2	Sequence 2, Appli
2	4797	100.0	921	13	US-10-054-680-2	Sequence 2, Appli
3	4784	99.7	927	14	US-10-275-116-2	Sequence 2, Appli
4	4686	97.7	927	9	US-09-804-474A-4	Sequence 4, Appli
5	4671	97.4	925	14	US-10-114-153-4	Sequence 4, Appli
6	4644	96.8	895	14	US-10-114-153-6	Sequence 6, Appli
7	4505.5	93.9	928	14	US-10-114-153-2	Sequence 2, Appli
8	3425.5	71.4	970	9	US-09-901-419-2	Sequence 2, Appli
9	3373.5	70.3	921	14	US-10-281-866-2	Sequence 2, Appli
10	3093	64.5	595	14	US-10-256-537-2	Sequence 2, Appli
11	3093	64.5	620	13	US-10-054-680-4	Sequence 4, Appli
12	2143.5	44.7	609	9	US-09-864-761-33429	Sequence 33429, A
13	2007	41.8	890	15	US-10-369-493-6319	Sequence 6319, Ap
14	1607	33.5	394	12	US-10-243-552-971	Sequence 971, App
15	1192	24.8	807	15	US-10-369-493-6148	Sequence 6148, Ap
16	1192	24.8	807	15	US-10-369-493-6149	Sequence 6149, Ap
17	424	8.8	91	9	US-09-864-761-33926	Sequence 33926, A
18	339	7.1	236	12	US-10-424-599-237064	Sequence 237064,
19	286	6.0	1081	16	US-10-408-765A-298	Sequence 298, App
20	258.5	5.4	644	15	US-10-353-690-18	Sequence 18, Appl
21	251.5	5.2	106	14	US-10-256-537-5	Sequence 5, Appli
22	243	5.1	161	12	US-10-424-599-228842	Sequence 228842,
23	239.5	5.0	661	13	US-10-094-214-5	Sequence 5, Appli
24	239.5	5.0	661	14	US-10-281-868-2	Sequence 2, Appli
25	239.5	5.0	661	15	US-10-391-399-17	Sequence 17, Appl
26	237.5	5.0	6304	14	US-10-147-026-16	Sequence 16, Appl
27	234.5	4.9	603	9	US-09-961-679-2	Sequence 2, Appli
28	232.5	4.8	546	12	US-10-276-774-2632	Sequence 2632, Ap
29	223.5	4.7	2092	14	US-10-147-026-12	Sequence 12, Appl
30	215.5	4.5	591	15	US-10-369-493-6463	Sequence 6463, Ap
31	215.5	4.5	591	15	US-10-369-493-6464	Sequence 6464, Ap
32	206	4.3	1577	14	US-10-219-834-150	Sequence 150, App
33	206	4.3	2780	12	US-10-423-483-2	Sequence 2, Appli
34	206	4.3	2780	15	US-10-220-587-2	Sequence 2, Appli
35	202	4.2	1615	14	US-10-219-834-149	Sequence 149, App
36	202	4.2	3838	12	US-10-262-511-162	Sequence 162, App
37	199	4.1	433	12	US-10-243-552-613	Sequence 613, App
38	194.5	4.1	152	13	US-10-094-214-4	Sequence 4, Appli
39	194.5	4.1	152	14	US-10-264-104-4	Sequence 4, Appli
40	194.5	4.1	152	14	US-10-256-537-4	Sequence 4, Appli
41	194.5	4.1	152	15	US-10-391-399-16	Sequence 16, Appl
42	194.5	4.1	500	14	US-10-264-104-2	Sequence 2, Appli
43	187	3.9	759	15	US-10-415-378-15	Sequence 15, Appl
44	186	3.9	461	15	US-10-104-047-2842	Sequence 2842, Ap
45	186	3.9	2753	12	US-10-262-511-160	Sequence 160, App

ALIGNMENTS

RESULT 1
 US-09-804-474A-2
 ; Sequence 2, Application US/09804474A
 ; Patent No. US20020119518A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
 PROTEINS,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000891
 ; CURRENT APPLICATION NUMBER: US/09/804,474A
 ; CURRENT FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 921
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-804-474A-2

Query Match 100.0%; Score 4797; DB 9; Length 921;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF	480
Db	421	KGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRVTSRGARTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETIVKTIRV	600

Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL 660
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Db 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKL 660

Qy 661 EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
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Db 901 SLWLLYILFATLEAYCYIKGF 921

RESULT 2

US-10-054-680-2

; Sequence 2, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 921

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-054-680-2

Query Match 100.0%; Score 4797; DB 13; Length 921;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGVLTVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
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Db 1 MAWLRLQPLTSAFLHFGVLTVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

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Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
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Db	181	IIGICVYVIPDGETRKHKL RVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
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Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD HAGIFTFECDTIH	540
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Db      901 SLWLLYILFATLEAYCYIKGF 921
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✓ RESULT 3

US-10-275-116-2

; Sequence 2, Application US/10275116

; Publication No. US20030096312A1

; GENERAL INFORMATION:

; APPLICANT: Merck Patent GmbH

; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein

; FILE REFERENCE: HNCX3CWWS

; CURRENT APPLICATION NUMBER: US/10/275,116

; CURRENT FILING DATE: 2002-11-01

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; NUMBER OF SEQ ID NOS: 2
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 2

; LENGTH: 927

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-275-116-2

Query Match 99.7%; Score 4784; DB 14; Length 927;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 921; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Db 1 MAWLRLQPLTSAFLHFGGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESC SGSSDCKEGVIL 60

[illegible]

Db 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSOEREVTIKKPNGE 120

Qy 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF I 180
| | | | |
| | | | |

Db 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

[illegible]

Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240

[illegible]

Db 241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

[illegible]

Db 301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLQDLVEMANYYYALSHQOKSRAFYRIOATR 360

Qy 361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFDFPCSYQCLENCGAVLLTVVR 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYOCLNCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF 480
| | | | |

Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||

Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
 |||

Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPV 654
 |||

Db 601 KIVDEEEYERQENFFIALGEPKWMERGISGVRFFKDVTDRKLTMEEEEAKRIAEMGKPV 660

Qy 655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
 |||

Db 661 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 720

Qy 715 EERLPSCFDYVMHFLTTFWVKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 774
 |||

Db 721 EERLPSCFDYVMHFLTTFWVKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 780

Qy 775 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
 |||

Db 781 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 840

Qy 835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLA 894
 |||

Db 841 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLA 900

Qy 895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||

Db 901 TTWLFVSLWLLYILFATLEAYCYIKGF 927

RESULT 4

US-09-804-474A-4

; Sequence 4, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 927

; TYPE: PRT

; ORGANISM: Rat

US-09-804-474A-4

Query Match

97.7%; Score 4686; DB 9; Length 927;

Best Local Similarity 96.8%; Pred. No. 0;
Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

Qy	1	MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
		:	
Db	181	IIGICVYVIPDGETRGIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGII IETEGDHPKGIEMDGKMMNSHFLDGN	300
		:	
Db	241	FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGII IETEGEHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
		:	
Db	301	LIPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
		:	
Db	361	MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
		:	
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
		:	
Db	481	FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDETIVKTIRV	600
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDETIVKTIRV	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPV	654
		:	
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISALLLSPEVTDRKLTMEEEEAKRIAEMGKPV	660
Qy	655	GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG	714
		:	
Db	661	GEHPKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDSG	720
Qy	715	EERLPSCFDYVMHFLTIVFWKVLVACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG	774
Db	721	EERLPSCFDYVMHFLTIVFWKVLVACVPPEYCHGWACFVVSILIIIGMLTAIIGDLASHFG	780
Qy	775	CTIGLKDSVTAVVFVAFGTSVDPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW	834

Db 781 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 840

Qy 835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
 |||||:|||||:|||||

Db 841 SVAAIYWAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLA 900

Qy 895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||||:|||||

Db 901 TTWLFVSLWLLYVLFATLEAYCYIKGF 927

RESULT 5

US-10-114-153-4

; Sequence 4, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Heyes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
 NUCLEIC ACIDS

; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

; FILE REFERENCE: 21402-322A

; CURRENT APPLICATION NUMBER: US/10/114,153

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: 60/281086

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282020

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282930

```
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-4
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Query Match          97.4%; Score 4671; DB 14; Length 925;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 896; Conservative 11; Mismatches 14; Indels 4; Gaps 1;
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Qy      1 MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        |||
Db      1 MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
        |||
Db     61 PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
        |||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
        |||
Db    181 IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300
        |||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQOKSRAFYRIQATR 360
        |||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQOKSRAFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        |||
Db    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        |||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
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Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHI	600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGE	656
		::: : : : : ::	
Db	601	KVIDDEAYEKNKNFYFIEMMGPRMVDMSFQKALLSPDRKLTMEEEEAKRIAEMGKPVLGE	660
Qy	657	HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE	716
Db	661	HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE	720
Qy	717	RLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT	776
Db	721	RLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT	780
Qy	777	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV	836
Db	781	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV	840
Qy	837	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT	896
Db	841	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT	900
Qy	897	WLFVSLWLLYILFATLEAYCYIKGF	921
Db	901	WLFVSLWLLYILFATLEAYCYIKGF	925

RESULT 6

US-10-114-153-6

; Sequence 6, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles

```

; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 6
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-6

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Query Match          96.8%; Score 4644; DB 14; Length 895;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 891; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      30 AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 89
       :|
Db      2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61

Qy      90 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 149
       ||
Db      62 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 121

Qy      150 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRGIKHLRVFFITA AW 209
       ||

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Db	122	LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFITA	181
Qy	210	SIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK	269
Db	182	SIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK	241
Qy	270	HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	329
Db	242	HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	301
Qy	330	KDLQDLVEMANYYYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	389
Db	302	KDLQDLVEMANYYYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	361
Qy	390	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT	449
Db	362	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT	421
Qy	450	EGTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	509
Db	422	EGTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	481
Qy	510	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTV	569
Db	482	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTV	541
Qy	570	EGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	629
Db	542	EGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	601
Qy	630	DVTDRLTMEEEEAKRIAEMGKPVLGHPKLEVIIEESYEFKTTVDKLIKKTNLALVVG	689
Db	602	DVTDRLTMEEEEAKRIAEMGKPVLGHPKLEVIIEESYEFKTTVDKLIKKTNLALVVG	661
Qy	690	HSWRDQFMEAITVSAAGDEDEDES GEERLPSCFDYVMHFLT VFWKVL FACVPPT EYCHGW	749
Db	662	HSWRDQFMEAITVSAAGDEDEDES GEERLPSCFDYVMHFLT VFWKVL FACVPPT EYCHGW	721
Qy	750	ACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	809
Db	722	ACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	781
Qy	810	YADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVC	869
Db	782	YADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVC	841
Qy	870	ISVLLYRRRPHLG GELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	921
Db	842	ISVLLYRRRPHLG GELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	893

RESULT 7

US-10-114-153-2

; Sequence 2, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 2
; LENGTH: 928

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-2

Query Match 93.9%; Score 4505.5; DB 14; Length 928;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 862; Conservative 37; Mismatches 21; Indels 9; Gaps 3;

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Qy      1 MAWLRLQPLTSAFLHFGVLTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||
Db      1 MAWLRLQPLTSAFLHFGVLTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      |||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      |||
Db    181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300
      |||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQOKSRAFYRIQATR 360
      |||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQOKSRAFYRIQATR 360

Qy    361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db    361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||
Db    481 FVRLSNVRIIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
      |||
Db    541 VSESIGVMEVKVLRRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Qy    601 KIVDEEEYERQENFFIALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPV 654
      |||
Db    601 KIVDDEEYKKNDFNFFIELGQPPQLKRGISALLNQGDGRKLTAEAAEARRIAEMGKPV 660

Qy    655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
      |||
Db    661 GENCRLVIIIEESYDFKNTVDKLIKKTNLALVIGTHSWREQFLEAITVS-AGDEEEEDG 719

Qy    715 --EERLPSCFDYVMHFLTTFWKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASH 772
```


RESULT 9
US-10-281-866-2
; Sequence 2, Application US/10281866
; Publication No. US20030091570A1

US-10-281-866-2

; Sequence 2, Application US/10281866

; Publication No. US20030091570A1

```
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MPI01-272P1RM
; CURRENT APPLICATION NUMBER: US/10/281,866
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-281-866-2
```

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Query Match          70.3%; Score 3373.5; DB 14; Length 921;
Best Local Similarity 71.0%; Pred. No. 9.3e-301;
Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;
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Qy      40 STGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99
      |||      | ||  |: ||:|:| |:|:|:| || :|:|:|:|:|:|:|:|:|:|
Db      39 STG----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM 94

Qy     100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
      |:|:|:|:|:|:|:|:|:| | |||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      95 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 154

Qy     160 FIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYM 219
      | |:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     155 FQAGELGPGTIVGSAAFNMFVVIACIYVIPAGESRKIKHLRVFFVTASWSIFAYVWLYL 214

Qy     220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIEG 279
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     215 ILAVFSPGVVQVWEALLTLVFFPVCVVFAMADKRLLFYKYVYKRYRTDPRSGIIIGAEG 274

Qy     280 DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRILKDLKQKHPEKDLDQ 334
      | || ||:| | : : | | | | | | | | | | | | | | | | | | | | |
Db     275 DPPKSIELDGTFGAE-APGELGGLGPGPAEARELDASRREVIQILKDLKQKHPDKDLEQ 333

Qy     335 LVEMANYYALSHQQKSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVHTDEPEDF 394
      || :|:|:| | | | | | | | | | | | | | | | | | | | | | | | |
Db     334 LVGIANYYALLHQQKSRAFYRIQATRLMTAGNVLRRHAADASRAAPAEAGAGEDE-DDG 392

Qy     395 ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSTMYVDYKTEDGSANAGADYEFTEGTVV 454
      |:|:|:| | | | | | | | | | | | | | | | | | | | | | | | |
Db     393 ASRIFFEPSLYHCLENCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDYEYSEGTLV 452

Qy     455 LKPGETQKEFSVGIIIDDDIFEDEHFFVRLSNVRIEEQ----PEEGMPPAIFNSLPLPR 510
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     453 FKPGETQKELRIGIIDDDIFEDEHFFVRLNLRVGDAQGMFEPDGG-----GRPK 503

Qy     511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
      | :| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     504 GRLVAPLLATVTILDDDHAGIFSQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD 563
```

Qy 571 GTAKGGGEDFEDTYGELEFKNDETVKTIIRVKIVDEEEYERQENFFIALGEPKWMERGISD 630
 |||:|||| :|| ||||| :|||:||||:||||:||||:||||:||||| ||:|:|:||||
 Db 564 GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFIELGQPQWLKRGISA 623

Qy 631 VT-----DRKLTMEEEEAKRIAEMGKPVLGEPKLEVIIEESYEFKTTVDKLIKKTNLA 684
 : ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 624 LLLNQGDGDRKLTAEEEEARRIAEMGKPVLGENCRLVIIIEESYDFKNTVDKLIKKTNLA 683

Qy 685 LVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHFLTTFWKVLFACVPP 742
 ||:|||||:||:||||| |||:|:| | |||||:|||||:|||||:|||||:|||||
 Db 684 LVIGTHSWREQFLEAITVS-AGDEEEEDGSREERLPSCFDYVMHFLTTFWKVLFACVPP 742

Qy 743 TEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK 802
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 743 TEYCHGWACFGVSILVIGLLTALIGDLASHFGCTVGLKDSVNAVVFVALGTSIPDTFASK 802

Qy 803 AAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF 862
 ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 803 VAALQDQCADASIGNVTGSNAVNVLGGLGVAWSVAAVYWAVQGRPFVVRTGTAFSVTLF 862

Qy 863 TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
 |:|||| |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 863 TVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWLLYILFASLEAYCHIRGF 921

RESULT 10

US-10-256-537-2

; Sequence 2, Application US/10256537
 ; Publication No. US20030162196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.
 ; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
 ; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
 ; FILE REFERENCE: MPI01-231P1RM
 ; CURRENT APPLICATION NUMBER: US/10/256,537
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/325,737
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 595
 ; TYPE: PRT
 ; ORGANISM: Homo sapien

US-10-256-537-2

Query Match 64.5%; Score 3093; DB 14; Length 595;
 Best Local Similarity 100.0%; Pred. No. 3e-275;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
 |||
 Db 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
 |||
 Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy 241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
 |||
 Db 241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy 301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQOKSRAFYRIQATR 360
 |||
 Db 301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQOKSRAFYRIQATR 360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 11

US-10-054-680-4

; Sequence 4, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 620

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-054-680-4

Query Match 64.5%; Score 3093; DB 13; Length 620;
 Best Local Similarity 100.0%; Pred. No. 3.2e-275;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETV 595
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETV 595
  
```

RESULT 12

US-09-864-761-33429

; Sequence 33429, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
 USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33429
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007281.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: EST_HUMAN HIT: AW452398.1, EVALUE 1.00e-49
; OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-33429

Query Match 44.7%; Score 2143.5; DB 9; Length 609;
Best Local Similarity 69.3%; Pred. No. 8.5e-188;
Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;

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Qy      1 MAWLRLQPLTSAFLHFGVLTVFLF--LNLRAEAGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | : : | : : | : | : | : |
Db     11 MRRLSLSPTFSMGFHLLVTVSLLFSHVDHVIAETEMEGETGE---CTGSYYCKKGV 66

Qy     59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPN 118
      | | | | | : : | | | | | : : | | | | | : : | | | | |
Db     67 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIDRFMSSIEVITSQEKEITIKKPN 126

Qy    119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
      | | : | | : | | | | | | | | | | | : | | | | | | | | |
Db    127 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 186

Qy    179 FIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      | | | : | | | : | | | | | | | | | | | | | | | | | |
Db    187 FIIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 246

Qy    239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
      | | | : | | : | | | | : | | | : | | | | | | | | | |
Db    247 FFFPICVVFVAVADRLLLFYKYVYKRYRAGKQGMIIIEHEDRPSSKTEIEMDGKVVNSH 306

Qy    296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ 348
      | | | | | | | | | : | | | | | | | | | : : : | : | | |
Db    307 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ 365

Qy    349 KSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      | | | | | | | | : | | | | | | : | | : | | | | : | |
Db    366 KSRAFYRIQATRLMTAGNILKRHAADQARKAVSMHEVNTTEVTENDPVSKIFFEQGTYQC 425

Qy    408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | : | | : : | | : : | | : | | | | | | |
Db    426 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG 485

Qy    468 IIDDDIFEDEHFFVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | : | | | | : : | : : | | | | | | | |
Db    486 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 542

Qy    528 HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      | | | | | | | | | | | : | | | | | | | | | : : : | | |
Db    543 HAGIFTFEVPVTHVSESIGIMEVKVLRITSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 602

Qy    588 EFKNDE 593
      | | : | |
Db    603 EFQNDE 608
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RESULT 13
US-10-369-493-6319
; Sequence 6319, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
 OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6319
 ; LENGTH: 890
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6319

Query Match 41.8%; Score 2007; DB 15; Length 890;
 Best Local Similarity 45.9%; Pred. No. 5.9e-175;
 Matches 416; Conservative 145; Mismatches 232; Indels 114; Gaps 13;

Qy	87	MFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP	146
		: : :	
Db	1	MFLGISIVADRFMSSIEVITSMERTIVVKRPGLDPMVQVRIWNDTVSNLTLMALGSSAP	60
Qy	147	EILLSLIEVCGHGFAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFIT	206
		: :	
Db	61	EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVWVIPKGEIRRQKHLDFVFCVT	120
Qy	207	AAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYR	266
		: :	
Db	121	ATWSVFAYVWLYLILAFFSPGEIEIWEAGALTFFIFFPLTVFTAYMADIKLIQNKFLPHRYR	180
Qy	267	TDKHRGIIIEGTEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK	326
		: :	
Db	181	RGSH-QOMIATEAEEMKMLE-----NGTQGDPAKKAFFEEHROEFIELMREIRKQ	228
Qy	327	HPEKDLQDLVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA-SSMSE	385
		: :	
Db	229	NPHITPTTELQKQAEYEMISRGPKSRAFYRVQATRRLIGGGDIVKKRIDKEHNKALDALVQ	288
Qy	386	VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD	445
		:	
Db	289	AQEKQSRDNTCKIFLDPAYHTVLESVGSFDVVVGRDGGPDGLTMVVDYFTEDGSANAGSD	348
Qy	446	YEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEG--MPPAIF	503
		: : : : : :	
Db	349	YIPVKGTLTFYPEDKHQKVTEIVVDDDDVFEDEHFFYLRLCNLRV---RTKDGIIDPTRI	405
Qy	504	NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVI	563
		:	
Db	406	GGLPV--AQLEMPNTATIMILDDDHAGVFGFEHDFQVVENCGLSLQMKRHSGARGKVI	463
Qy	564	VPFRTVEGTAKGGGEDFEDTYGELEFKNDETIVTKIRVKIVDEEEYERQENFFIALGEPKW	623
		:	
Db	464	IPFRTVEGTA-SADKHFEMKEGEIVFEDNQTEALVEIGIVDTEQYERSDYFYIELSPPIW	522

Qy	624	-----MERGISDVTDRK-----LTMEEEEA	643
		: : :	
Db	523	AKKMNDLSRIQERFQRRMERKRGSSVASESKDSNTENALAPAEEKSTRAASVDLLQPSSDP	582
Qy	644	KR-----IAEMGKPVLGHPKL	660
		:	
Db	583	RRSSQTNSPHLTSRFRNRLGSWIAGMKGGNGDDEVTTSLTPSQLEIAEMGKPRLGFTKC	642
Qy	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDED----ESGEE	716
		:: : :: ::: : : : :	
Db	643	QITIRESKEFQGI VDRMIKNANTRIMLGTHSWREQFMEALVVSAGDDDDDEGEDGEDGEE	702
Qy	717	R---LPSCFDYVMHFLT VFWKVL FACVPPT EYCHGWACFAVSILII GMLTAIIGDLASHF	773
		: : : : : : : : :	
Db	703	KEPEEPGCM DYVMHVLT VPWKLT FATIPPTDYFGGWATFVVAIFMIGVLTAVVGDLASQF	762
Qy	774	GCTIGLKDSVTAVVFVAFGTSVPD TFASKAAALQDVYADASIGNVTGSNAVN VFLGIGLA	833
		: : : : : : : :	
Db	763	GCWVGLKDAVTAISFVALGTSVPD TFASKVSAVQDKYADNAVGNVTGSNAVN VFLGIGIA	822
Qy	834	WSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKL	893
		: : : : : : :	
Db	823	WSMAAIYHWNQGTKFLVDPGNLGF SVLIFCTEAVLCIIVLVLRNKKVGGELGGPIALRL	882
Qy	894	ATTWLFV	900
		:	
Db	883	T---IFV	886

US-10-243-552-971

; Sequence 971, Application US/10243552

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Wang, Zhiwei

; APPLICANT: Ma, Yunging

; TITLE OF INVENTION: Polypeptides

; CURRENT APPLICATION NUMBER: US/10/243,552

; PRIOR APPLICATION NUMBER: US 60/322,511

; PRIOR APPLICATION NUMBER: PCT/US00/35017

; PRIOR APPLICATION NUMBER: US 09/488,725

; PRIOR APPLICATION NUMBER: US 09/552,317

; PRIOR APPLICATION NUMBER: PCT/US01/02623

; PRIOR APPLICATION NUMBER: US 09/491,404


```
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6148
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6148
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Query Match          24.8%; Score 1192; DB 15; Length 807;
Best Local Similarity 33.6%; Pred. No. 5.6e-100;
Matches 302; Conservative 150; Mismatches 320; Indels 126; Gaps 20;
```

```
Qy      47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
      | | : | | |:: | : | | | | |:: | | | | | |
Db      2 SSSANLTCKNGILI-----PALETTPRNAILYLAGLFYCFGLGIAIAADIFMCSIEQIT 54

Qy     107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      | :: | : | | : | | | | | | | | | | | | | | | | |
Db      55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDVRIWNPTVANLTLMALGSSAPEILLSIIEI 114

Qy     156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYI 215
      | : | | | | | | | | | | | | | | | | | | | | |
Db     115 VGNGFKAGDLGPGTIVGSAAFNLFCISAICVFAV-GTQTKRIELRVFVVTAFFGT FayI 173

Qy     216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTD----- 268
      | :: : | | : | | | | | | | | | | | | | | | |
Db     174 WVFLVLIVITPNVVDVWEAILTLFFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy     269 -KHRGIIIETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRRMIRILKDL 323
      : | | : | | : : : | | : : : : | | | | | : :
Db     229 AQHDGKV----DDQPEKLSDEIKKWASNLNKEENDVIVDATPSVDTVR----RWTRSI 280

Qy     324 KQKHPEKDLQVLVEMANYYYALSHQOKSRAFYRIQATRMGTAGNILKKHAAEQAKKASSM 383
      : | : : : | | : | | | | | : : : : | | | :
Db     281 SHTYPSLSDEDQAKILAYRVSRMTMSHDRLYYRIRAIRQLSSS---WRKSEEEVLKMEHQ 337

Qy     384 SEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAG 443
      | | : | | | : | | : | | | | | | | | | |
Db     338 ES--TDSASRRKTFVEFSARVYRVDATDET VSLKIERK-GNMESKFTVSYATVNGLAKKD 394

Qy     444 ADYEFTEGT VVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIF 503
      : : | | : | | | | | : : : : : : : : : :
Db     395 LNFLFKSETLQFNPGELHKTISIQLINAANWRPNDFVYVHLKIQDVDED----- 443

Qy     504 NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH-VSESIGVMEVKVLR TSG-ARGT 561
      : | : | | | | | | | | | | | | | |
Db     444 -----SKICLGA-----CNVAHVVKENAGFSRSFVTRRGGLKKP 478
```

Qy	562	VIVPFRVTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEP	621
		: : : : : : :: :	
Db	479	LQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYEKYIDIDVIDDKMDEKDEAFIIEI--L	536
Qy	622	KWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFK--TTVDKLIK	679
		: : : :	
Db	537	KVDEPGVSIGTRRKATI-----TIISDDNVLKNITNVRKLMG	573
Qy	680	KTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWKVL FAC	739
		: : : : : : : :	
Db	574	HYMRQLRPGKATWKEQILNAVSVNA-----GDLANATVSDCILHALAFPWKFAFAF	624
Qy	740	VPPTYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTF	799
		: : : : : : : : : : : : :	
Db	625	LPPPTIFYGYPCFVVALIGIGLVTAVVGDVASIFGCMVGLKDAVTAITLVALGTSLPDTF	684
Qy	800	ASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSV	859
		: : : : :	
Db	685	ASKIAAESDDTADNAVGNVTGSNSVNVLGLGLPWVIASLYWASKGESFRVDAGDLGFSV	744
Qy	860	TLFTIFAFVCISVLLYRRRPHL--GGELGGPRGCKLATTWLFVSLWLLYILFATLEAY	915
		: : : : : : : : : : :	
Db	745	TVFMICSVLFLVVLVLRRLKKAFGOGELGGPFGTKTLSALFFVGLWIVYVGLSIWKMY	802

Search completed: June 24, 2004, 16:17:29
Job time : 53.8014 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:06:37 ; Search time 49.0084 Seconds
(without alignments)
5929.434 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	4768.5	99.4	924	4	Q96QG1	Q96qg1 homo sapien
2	4692	97.8	921	11	Q7TS90	Q7ts90 mus musculu
3	4671	97.4	925	4	Q96QG2	Q96qg2 homo sapien
4	4563.5	95.1	928	11	Q8VHJ8	Q8vhj8 mus musculu
5	4019	83.8	771	4	Q86Y47	Q86y47 homo sapien
6	3458.5	72.1	934	6	Q97801	Q97801 macaca mula
7	3442.5	71.8	941	6	Q28662	Q28662 oryctolagus
8	3437.5	71.7	941	6	Q9TS14	Q9ts14 oryctolagus
9	3427.5	71.5	934	11	Q9R238	Q9r238 rattus norv
10	3425.5	71.4	934	11	Q9WU30	Q9wu30 rattus norv
11	3417	71.2	957	11	Q9R239	Q9r239 rattus norv
12	3409.5	71.1	962	11	Q924Y2	Q924y2 rattus norv
13	3406	71.0	969	11	Q9WU29	Q9wu29 rattus norv
14	3357	70.0	921	11	Q8K596	Q8k596 mus musculu
15	3290.5	68.6	968	13	Q9PT19	Q9pt19 oncorhynch
16	3229	67.3	963	13	Q7T3T7	Q7t3t7 oreochromis
17	3191.5	66.5	940	11	O35157	O35157 mus musculu
18	3012	62.8	595	11	Q9EPU8	Q9epu8 mus musculu
19	2896	60.4	607	11	Q8BXN1	Q8bxn1 mus musculu
20	2652	55.3	706	11	Q8BXB3	Q8bxb3 mus musculu
21	2533	52.8	892	5	O02196	O02196 loligo opal
22	2203.5	45.9	925	5	O45630	O45630 caenorhabdi
23	2203.5	45.9	925	5	Q8MYP6	Q8myp6 caenorhabdi
24	2176.5	45.4	975	5	Q8MYP5	Q8myp5 caenorhabdi
25	2160.5	45.0	793	4	Q9H021	Q9h021 homo sapien
26	2156.5	45.0	602	6	Q9TV05	Q9tv05 macaca mula
27	2130.5	44.4	950	5	Q9VDG5	Q9vdg5 drosophila
28	2130.5	44.4	950	5	Q24413	Q24413 drosophila
29	2128.5	44.4	600	11	Q91ZJ7	Q91zj7 mus musculu
30	2126.5	44.3	600	11	Q9ET74	Q9et74 mus musculu
31	2119	44.2	950	5	O18367	O18367 drosophila
32	2102	43.8	583	13	Q91850	Q91850 xenopus lae
33	2093.5	43.6	950	5	Q8I7I8	Q8i7i8 caenorhabdi
34	2001.5	41.7	880	5	Q21609	Q21609 caenorhabdi
35	1912.5	39.9	560	13	Q91849	Q91849 xenopus lae
36	1679	35.0	323	4	Q86TQ9	Q86tq9 homo sapien
37	1278	26.6	254	13	Q9YH83	Q9yh83 gallus gall
38	1192	24.8	807	5	Q21895	Q21895 caenorhabdi
39	1105.5	23.0	263	13	Q9YGE0	Q9yge0 oncorhynch
40	1046.5	21.8	263	13	Q9YH84	Q9yh84 gallus gall
41	1038	21.6	264	13	Q9YGE1	Q9yge1 oncorhynch
42	970.5	20.2	267	13	Q9YGE2	Q9yge2 oncorhynch
43	835	17.4	405	5	Q8I7I7	Q8i7i7 caenorhabdi
44	660	13.8	199	11	Q8R505	Q8r505 mus musculu
45	659	13.7	152	11	Q80XU9	Q80xu9 rattus sp.

ALIGNMENTS

RESULT 1

Q96QG1

ID	Q96QG1	PRELIMINARY;	PRT;	924 AA.
AC	Q96QG1;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		

DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabellini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
RT 8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ304853; CAC40985.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
SQ SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;

Query Match 99.4%; Score 4768.5; DB 4; Length 924;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 918; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy	1	MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHKLRFVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVLVEMANYALSHQQKSRAFYRIQATR	360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGISDV---TDRKLTMEEEEAKRIAEMGKPVLGHEH 657
 ||| : |||
 Db 601 KIVDEEEYERQENFFIALGEPKWMERGISALLSPDRKLTMEEEEAKRIAEMGKPVLGHEH 660

Qy 658 PKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEER 717
 |||
 Db 661 PKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEER 720

Qy 718 LPSCFDYVMHFLT VFWKVL FACVP PTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTI 777
 |||
 Db 721 LPSCFDYVMHFLT VFWKVL FACVP PTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTI 780

Qy 778 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 837
 |||
 Db 781 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 840

Qy 838 AIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGE LGGPRGCKLATTW 897
 |||
 Db 841 AIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGE LGGPRGCKLATTW 900

Qy 898 L FVSLWLLYILFATLEAYCYIKGF 921
 |||
 Db 901 L FVSLWLLYILFATLEAYCYIKGF 924

RESULT 2

Q7TS90

ID Q7TS90 PRELIMINARY; PRT; 921 AA.
 AC Q7TS90;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Slc8a3 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||:||||
 Db 421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||:|||| ||| |||
 Db 481 FVRLSNVRVEEQQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDAYGELEFKNDET VKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEPK 660
 |||:||||:||||
 Db 601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTVEEEEAKRIAEMGKPVLGEPK 660

Qy 661 EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
 |||:||||
 Db 661 EVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAGDEDEDESGEERLPS 720

Qy 721 CFDYVMHFLT VFWKVL FACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLK 780
 |||
 Db 721 CFDYVMHFLT VFWKVL FACVPPEYCHGWACFVVSILIIIGMLTAIIGDLASHFGCTIGLK 780

Qy 781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIY 840
 |||
 Db 781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIY 840

Qy 841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
 ||:||||:||||
 Db 841 WAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLATTWLFV 900

Qy 901 SLWLLYILFATLEAYCYIKGF 921
 |||
 Db 901 SLWLLYILFATLEAYCYIKGF 921

RESULT 3

Q96QG2

ID Q96QG2 PRELIMINARY; PRT; 925 AA.
 AC Q96QG2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium/calcium exchanger SCL8A3.
 GN SCL8A3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bortoluzzi S.;

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHV 600
 |||||||||||||||||||||||||||||||||||||||||||||||||||| :
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHI 600

Qy 601 KIVDEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGE 656
 |:::| ||: ||:| : | : : ||||||||||||||||||||
 Db 601 KVIDDEAYEKNKNFYFIEMMGPRMVDMSFQKALLSPDRKLTMEEEEAKRIAEMGKPVLGE 660

Qy 657 HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE 716
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 HPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESCEE 720

Qy 717 RLPSCFDYVMHFLTTFWVKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCT 776
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 RLPSCFDYVMHFLTTFWVKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCT 780

Qy 777 IGLKDSVTAVVFVAFGTSPVDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV 836
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 IGLKDSVTAVVFVAFGTSPVDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV 840

Qy 837 AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT 896
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT 900

Qy 897 WLFVSLWLLYILFATLEAYCYIKGF 921
 ||||||||||||||||||||
 Db 901 WLFVSLWLLYILFATLEAYCYIKGF 925

RESULT 4

Q8VHJ8

ID Q8VHJ8 PRELIMINARY; PRT; 928 AA.
 AC Q8VHJ8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium/calcium exchanger.
 GN SLC8A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
 RA Kraev A.;
 RT "Towards complete inventory of calcium transporters of the house
 RT mouse.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF453257; AAL39160.1; -.
 DR MGD; MGI:107976; Slc8a3.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

Db 601 KVIDDKAYEKNKNYVIEEMGPRMVDMSVQKALLLSPEVTDKRLTVEEEEAKRIAEMGKPV 660

Qy 654 LGEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDES 713
 |||||:|||||

Db 661 LGEHPKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAGGDEDEDES 720

Qy 714 GEERLPSCFDYVMHFLTTFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHF 773
 |||||:|||||

Db 721 GEERLPSCFDYVMHFLTTFWKVLFACVPPTEYCPGWACFVVSILIIGMLTAIIGDLASHF 780

Qy 774 GCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLA 833
 |||||:|||||

Db 781 GCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLA 840

Qy 834 WSVAAIYWALQGQEFHVSAGTLAFSVTLFTTIFAFVCISVLLYRRRPHLGGEELGGPRGCKL 893
 |||||:|||||

Db 841 WSVAAIYWAMQGQEFHVSAGTLAFSVTLFTTIFAFVCLSVLLYRRRPHLGGEELGGPRGCKL 900

Qy 894 ATTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||||

Db 901 ATTWLFVSLWLLYILFATLEAYCYIKGF 928

RESULT 5

Q86Y47

ID Q86Y47 PRELIMINARY; PRT; 771 AA.

AC Q86Y47;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Na⁺/Ca²⁺ exchanger isoform 4 (Fragment).

GN NACAIS4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Lindgren R.M., Bongcam-Rudloff E., Nister M., Heller S.;

RT "Homo sapiens partial mRNA for Na⁺/Ca²⁺ exchanger isoform 4.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ508602; CAD48420.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR InterPro; IPR003644; Calx_beta.

DR InterPro; IPR004837; NaCa_Exmemb.

DR InterPro; IPR004836; Na_Ca_Ex.

DR Pfam; PF03160; Calx-beta; 2.

DR Pfam; PF01699; Na_Ca_Ex; 1.

DR PRINTS; PR01259; NACAEXCHNGR.

DR SMART; SM00237; Calx_beta; 2.

DR TIGRFAMs; TIGR00845; caca; 1.

FT NON_TER 1 1

SQ SEQUENCE 771 AA; 86146 MW; A204AAA48A52ED8B CRC64;

Query Match 83.8%; Score 4019; DB 4; Length 771;
Best Local Similarity 99.7%; Pred. No. 9.2e-285;
Matches 769; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	151	SLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKLRFVFFITAAWS	210
Db	1	SLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKLRFVFFITAAWS	60
Qy	211	IFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKH	270
Db	61	IFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKH	120
Qy	271	RGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	330
Db	121	RGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	180
Qy	331	DLDDLQVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDE	390
Db	181	DLDDLQVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDE	240
Qy	391	PEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	450
Db	241	PEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	300
Qy	451	GTIVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	510
Db	301	GTIVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	360
Qy	511	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE	570
Db	361	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE	420
Qy	571	GTAKGGGEDFEDTYGELEFKNDETVKTIKIVDEEEYERQENFFIALGEPKWMERGISD	630
Db	421	GTAKGGGEDFEDTYGELEFKNDETVKTIKIVDEEEYERQENFFIALGEPKWMERGISD	480
Qy	631	VTDRKLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTH	690
Db	481	VTDRKLTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTH	540
Qy	691	SWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTTFWKVLFACVPPTTEYCHGWA	750
Db	541	SWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTTFWKVLFACVPPTTEYCHGWA	600
Qy	751	CFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVY	810
Db	601	CFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVY	660
Qy	811	ADASIGNVTGSNAVNVLGIGLAWSVAAYWALQGQEFHVSAGTLAFSVTLFTIFAFVCI	870
Db	661	ADASIGNVTGSNAVNVLGIGLAWSVAAYWALQGQEFHVSAGTLAFSVTLFTIFAFVCI	720
Qy	871	SVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	921
Db	721	SVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	771

097801

Query Match 72.1%; Score 3458.5; DB 6; Length 934;
Best Local Similarity 71.8%; Pred. No. 1.1e-243;
Matches 676; Conservative 108; Mismatches 129; Indels 29; Gaps 10;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKE	58
		: : : : : : : :	
Db	1	MRRLSLSPTFSMGFHLLVIVALLFSHVDYVIAETEME	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVC	178
		: : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVC	176
Qy	179	FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
		: : : : : : : :	
Db	177	FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236

DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 934 AA; 104166 MW; C04E0D8A75633DDC CRC64;

Query Match 71.5%; Score 3427.5; DB 11; Length 934;
 Best Local Similarity 70.9%; Pred. No. 2.1e-241;
 Matches 671; Conservative 107; Mismatches 127; Indels 41; Gaps 11;

Qy 4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
 ||| : : | || | | || ||: ||| ||
 Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
 :||||| |:| | |||| | ||||:||||| ||||:|||||
 Db 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113

Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
 |||||: |||:||||| |||||:||||| |||||:|||||
 Db 114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173

Qy 176 FNMFIIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEG 235
 ||||| :|||:||||| ||||:||||| ||||:||||| ||||:|||||
 Db 174 FNMFIIALCVYVVPDGETRKKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEG 233

Qy 236 LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTDHPKG---IEMDGKMM 292
 || ||||:|: ||||:|||||:|:| | ||:| | | ||||:|
 Db 234 LTFFFFPICVVFVAVVADRRLLFYKYVYKRYRAGKQGRGMIIIEHGEDRPASKTEIEMDGKV 293

Qy 293 NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQVLVEMANYYALS 345
 ||| ||| || || | | | :||| |||:|||||:|:| | ||
 Db 294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy 346 HQQKSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
 ||||| ||||:|||||:||||:| | ||: | | | :||||: |
 Db 353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy 405 YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
 ||||| | ||:|:|:|: | : ||:|:|:|:|:|:|:|:|:|:|:|
 Db 413 YQCLENCGTVALTIIRRGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy 465 SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
 ||||| ||||:| | ||||: | |:| | : | | | ||:|
 Db 473 RVGIIDDDIFEEDENFLVHLSNVRSSEVSEEDG---ILDSNHVSAIACLGSPNTATITI 528

Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
 ||||| ||||:||||| ||||:||||| ||:|:|:|:|:|:|:|
 Db 529 FDDDHAGIFTFEFPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588

DR PROSITE; PS50076; DNAJ_2; 1.
SO SEQUENCE 934 AA; 104210 MW; 054D06E9179098B5 CRC64;

Qy	4	LRLQPLTSAFLHFGSLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKJARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	17
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILPSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
Db	174	FNMFIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
Db	234	LTFFFFFPICVVFVAWVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
Db	294	NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMMTGAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNIIKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG---ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIIIPYKTIEGTARGGGEDFEDT	588
Qy	584	YGELEFKNDETVKTIRVKIVDEEYERQENFFIALGEPKWMERGI-----SDVTDK-	635
Db	589	CGELEFQNDIEVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTTEEYDDKQP	648
Qy	636	LTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQ	695
Db	649	LTSKEEEEERRIAEMGRPILGHTKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHNSWREQ	708
Qy	696	FMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTTFVKVLFACVPPTTEYCHGWACFAVS	755

Db	709	FIEAITVSAGEDDDDDDECGEKLPSCFDYVMHFLTTFVKVLFVAFVPPTEYWNGWACFIVS	768
Qy	756	ILIIGMLTAIIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI	815
		: :	
Db	769	ILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASI	828
Qy	816	GNVTGSNAVNVLFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLY	875
		: : : : :	
Db	829	GNVTGSNAVNVLFLGIGVAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLly	888
Qy	876	RRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	921
		: : :	
Db	889	RRRPEIGGELGGPRTAKLITSSLEVLWLLYIFFSSLEAYCHIKGF	934

Q9R239

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ID      Q9R239          PRELIMINARY;          PRT;    957 AA.
AC      Q9R239;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Na+/Ca2+-exchanging protein.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Dahl/Rapp S Sprague-Dawley;
RA      Unlap M.T., Bell P.D.;
RT      "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT      Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF109164; AAD23387.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR      GO; GO:0006816; P:calcium ion transport; IEA.
DR      InterPro; IPR003644; Calx_beta.
DR      InterPro; IPR001623; DnaJ_N.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      InterPro; IPR004836; Na_Ca_Ex.
DR      Pfam; PF03160; Calx-beta; 2.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      PRINTS; PR01259; NACAEXCHNGR.
DR      SMART; SM00237; Calx_beta; 2.
DR      TIGRFAMs; TIGR00845; caca; 1.
DR      PROSITE; PS50076; DNAJ_2; 1.
SQ      SEQUENCE      957 AA;  106724 MW;  7A146630451EAA7E CRC64;

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Qy 4 LRLQPLTSAFLHFGVLTVFLF-----NGLRAEAGSGDVPSTGQNNESCSGSSDCK 55
||| : : | || | | || ||: |:|| ||
Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIK	115
		: : : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : : : : :	
Db	174	FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIFLSVSSPGVVEVWEGL	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG--IEMDGKMM	292
		: : : : : : :	
Db	234	LTFFFFPICVVFVAVADRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS	345
		: : : : : : :	
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRIFYRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : : : :	
Db	353	QQQKSRIFYRIQATRLMTGAGNILLKHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCNAVLLTVVRKGGDMSTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		: : : : : : : : : : : : : :	
Db	413	YQCLENCCTVALTIIRGGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : : :	
Db	473	RVGIIDDDIFEEDENFLVHLSNVRSSEVSEEDG---ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
		: : : : : : : : :	
Db	529	FDDDHAGIFTFEPPVTHVSESIGIMEVKVLRITSGARGNVIIPYKTIEGTARGGGGEDFEDT	588
Qy	584	YGELEFKNDETIVKTIRVKIVDEEEYERQENFFIALGEPKWMERG-----	627
		: : : : : : :	
Db	589	CGELEFQNDIVKIITIRIFDREEYEKECSFSLVLEPKWIRRGMKGGFTLTGQPVFRKV	648
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKT	672
		: : : : : : : :	
Db	649	HARDHPISTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIIEESYEFKS	708
Qy	673	TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTTF	732
		: : : : : : : : : : :	
Db	709	TVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDECGEKLPSCFDYVMHFLTTF	768
Qy	733	WKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFAFG	792
		: : : : : : : :	
Db	769	WKVLFACVPPEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFAFG	828
Qy	793	TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAIIYWALQGQEFHVSA	852
		: : : : :	
Db	829	TSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIIYAANGEQFKVSP	888

Qy 853 GTLAFSVTLFTIFAFVCISVLLYRRRPHLGGEELGGPRGCKLATTWLFVSLWLLYILFATL 912
 |||||: : ||||| :||| | | : || | ||||| |:|
 Db 889 GTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSL 948
 Qy 913 EAYCYIKGF 921
 ||||:||||
 Db 949 EAYCHIKGF 957

RESULT 12

Q924Y2

ID Q924Y2 PRELIMINARY; PRT; 962 AA.
 AC Q924Y2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Na+/Ca2+ exchanger.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Unlap M.T., Bell P.D., Williams I.;
 RT "Cloning and expression of a mesangial cell Na+/Ca2+ exchanger from
 RT Sprague-Dawley rats.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY033398; AAK52307.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 962 AA; 107270 MW; 1AA422ED25964182 CRC64;

Query Match 71.1%; Score 3409.5; DB 11; Length 962;
 Best Local Similarity 69.0%; Pred. No. 4.6e-240;
 Matches 672; Conservative 105; Mismatches 128; Indels 69; Gaps 11;

Qy 4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
 ||| : : | || | | || ||: ||| ||
 Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
 Qy 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
 :||| ||| ||||| |||||:||||| |||||:||||| |||
 Db 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
 Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175

Db	114	KPNGETTKTTTVRIWNETVSNLTLMALGSSAPEILPSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWVEGL	235
Db	174	FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWVEGL	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMM	292
Db	234	LTFFFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYSALS	345
Db	294	NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQOKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSGVSEDG----ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRVTSARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRVTSARGNVIIIPYKTIEGTARGGGEDFEDT	588
Qy	584	YGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERG-----	627
Db	589	CGELEFQND EIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTGKKMYGQP	648
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVIIEES	667
Db	649	VFRKVHARDHPI PSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIEES	708
Qy	668	YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMH	727
Db	709	YEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDCEGEEKLPSCFDYVMH	768
Qy	728	FLT VFWKVLFA CVPPTEYCHGWACFAVSILIGMLTAIGDLASHFGCTIGLKDSVTAVV	787
Db	769	FLT VFWKVLFA FVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVV	828
Qy	788	FVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQE	847
Db	829	FVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQ	888
Qy	848	FHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSLWLLYI	907
Db	889	FKVSPGTLAFSVTLFTIFAFINVGVLRYRRRPEIGELGGPRTAKLLTSSLFVLLWLLYI	948
Qy	908	LFATLEAYCYIKGF	921

RESULT 13

Q9WU29

ID Q9WU29 PRELIMINARY; PRT; 969 AA.
 AC Q9WU29;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Na⁺/Ca²⁺-exchanging protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Unlap M.T., Bell P.D.;
 RT "cDNA cloning of two Na⁺/Ca²⁺ exchangers in mesangial cells from
 RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF109165; AAD23388.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 969 AA; 108037 MW; 1D64F6073D3C9CF5 CRC64;

Query Match 71.0%; Score 3406; DB 11; Length 969;

Best Local Similarity 68.5%; Pred. No. 8.3e-240;

Matches 672; Conservative 105; Mismatches 128; Indels 76; Gaps 11;

Qy 4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
 ||| : : | || | | || ||: |:|| ||
 Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
 :||||| |:| | |||| | ||||:||||||| |||||:|:| |||
 Db 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113

Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
 |||||: ||:|:||||||| ||||| | ||||| |||||
 Db 114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILPSVIEVCGHNF TAGDLGPSTIVGSAA 173

Qy 176 FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
 ||||| :|||:||||||| |||||:||||| ||||:|||||
 Db 174 FNMFIILALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233

Qy	236	LTLLLLPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---	IEMDGKMM	292
Db	234	LTFFFFPICVVFVAVDRLLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV		293
Qy	293	NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQLVEMANYALS		345
Db	294	NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS		352
Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS		404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT		412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF		464
Db	413	YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI		472
Qy	465	SVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI		523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSGVSEDG----ILDSNHVSAIACLGSPNTATITI		528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTEGTAKGGGEDFEDT		583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIIPYKTIEGTARGGGEDFEDT		588
Qy	584	YGELEFKNDETVKTIIRVKIVDEEEYERQENFFIALGEPKWMERG-----		627
Db	589	CGELEFQNDIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKALLLNELGGFTLTG		648
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHEHPKL		660
Db	649	KKMYGQPVFRKVHARDHIPSTVISISEYDDKQPLTSKEEEERRIAEMGRPILGEHTKL		708
Qy	661	EVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS		720
Db	709	EVIIIEESYEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDECGEELPS		768
Qy	721	CFDYVMHFLTTFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIGDLASHFGCTIGLK		780
Db	769	CFDYVMHFLTTFWKVLFACVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLK		828
Qy	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY		840
Db	829	DSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIY		888
Qy	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFV		900
Db	889	HAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLRYRRRPEIGELGGPRRTAKLLTSSLFV		948
Qy	901	SLWLLYILFATLEAYCYIKGF	921	
Db	949	LLWLLYIFFSSLEAYCHIKGF	969	


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OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RX      MEDLINE=99447215; PubMed=10516099;
RA      Xue X.H., Hryshko L.V., Nicoll D.A., Philipson K.D., Tibbits G.F.;
RT      "Cloning, expression, and characterization of the trout cardiac
RT      Na(+)/Ca(2+) exchanger.";
RL      Am. J. Physiol. 277:C693-C700(1999).
DR      EMBL; AF175313; AAF06363.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR      GO; GO:0006816; P:calcium ion transport; IEA.
DR      InterPro; IPR003644; Calx_beta.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      InterPro; IPR004836; Na_Ca_Ex.
DR      Pfam; PF03160; Calx-beta; 2.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      PRINTS; PR01259; NACAEXCHNGR.
DR      SMART; SM00237; Calx_beta; 2.
DR      TIGRFAMs; TIGR00845; caca; 1.
SQ      SEQUENCE   968 AA;  107504 MW;  5F8A92824B26DA36 CRC64;

```

Qy	19	VTFLVFLNGLRAEAGGSGDVPSTG-----QNNESC-SGSSDCKEGVILPIWYPENPSL	70
Db	18	VLLAVFSSEIKFVTAGNSN-PSLGTNSSIGNQTNNKKCDSDVDECKVGVILPIWLPENTSF	76
Qy	71	GDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWN	130
Db	77	GDKLARATVYFVALFYMFLGVSIIADRFMASIEVITSQEREITIKKPNGEKVTTTVRIWN	136
Qy	131	ETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GD LGPSTIVGSAAFNMFIIGICVYVIP	190
Db	137	ETVSNLTLMALGSSAPEILLSVVEVCGHNFDAGD LGPNTIVGSAAFNMFVIIGFCVSVIP	196
Qy	191	DGETRKIKHLRVFFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFFFPVCVLLAWV	250
Db	197	DGEHRKVKHLRVFFVTATWSIFAYTWLYLILAVISPGIVQVWEGLVTLFFFP LCVGMAYV	256
Qy	251	ADKRLLFYKYMHHKKYRTDKHRGII IETEGD---HPKGIEMDGKMMNSH-FLDGNLVPLE	305
Db	257	ADRRLLVYKMYMKRYRAGKRRGVIIETEGEAQIPSKMDIEMDGKMLNSESFMDG-AMGFD	315
Qy	306	GKEVD--ESRREMIRILKDLKQKHPEKDL DQLVEMANYALSHQQKSRAFYRIQATRMMT	363
Db	316	EKDLDEEEARREMVRIKELKQKHPEKETEQ LI ELANYQVLTQQQKSRAFYRCQATRIMT	375
Qy	364	GAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVLLTVVRKG	422
Db	376	GAGNVLKKHAADQARKAVGAYEIRSEVSEND FSSKVFFDPGT YQCLENCGTVALNVVRLG	435
Qy	423	GDMSKTMVVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVGIIDDDIFEDEHFFV	482

Db 436 GDLTNTVSVEYRTEDGTANAGSDYQFTEGVVVFNPGETEKEIRIDIIDDDIFEDEHFLV 495
 Qy 483 RLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVS 542
 ||||:: | | | | | | | | | | | | | | : : |
 Db 496 HLSNVKVI SEGTGYVQ PRA--NHLD-TLAGLGLPCSATVTIFDDDHAGIFTFEPPVMTIS 552
 Qy 543 ESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKI 602
 ||||:||||| ||||| :||::||| ||||| ||||| ||||| : ||| :||:: |
 Db 553 ESIGMMEVKVLRTSGARGLVVVPYKTMEGTAKGGGEDFEDTHGALEFQND EIFKSIQINI 612
 Qy 603 VDEEEYERQENFFIALGEPKWMERGISDVTDRK----- 635
 :||:||||: :|||: :|||: :| :::||
 Db 613 IDDEEYEKNKNFFLEMGEPOLLE-----MSERKAVLLQEIGGFVK TGRDVYRKVQGRDNP 667
 Qy 636 -----LTMEEEEAKRIAEMGKPV LGHPKLEVIIEESYEFKTTVDKLIK 679
 | : :|| :||| ||| :||| :||| ||||| ||||| |||||
 Db 668 VPATIISLAEEGDEEALSKKEEEEERRIAEMGRPTLGHEVKLEV VIEESYEFKNTVDKLIK 727
 Qy 680 KTNLALVVGTHSWRDQFMEAITVSAAGDEDEDES GEERLPSCFDYVMHFLT VFWKVLFAF 739
 |||||::||:||| ||||| |||:||| |||:||||| ||||| :|||
 Db 728 KTNLALLIGTNSWRQQFMEAITVS-SGDDDEDEC GEEKLPSCFDYVMHFLT VFWKLLFAF 786
 Qy 740 VPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTF 799
 ||||:| :||| ||| :||| ||| :||| ||| :||| ||| :||| |||
 Db 787 VPPTDYWNGWACFVVSISMI GLLTAFIGDLASHFGCTVGLKDSVTAVVFVALGTSVPDTF 846
 Qy 800 ASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA AIYWALQGQEFHVSAGTLAFSV 859
 ||| ||:|| ||| ||||| ||||| :||:||| :| :| | |||||
 Db 847 ASKVA AIQDQYADAFIGNVTGSNAVNVFLGIGVAWSIAAIYHNSKGNDFRVDPGTLAFSV 906
 Qy 860 TLFTIFAFVCISVLLYRRRPHLG GELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIK 919
 ||||| ||| :||:||| :||| ||| :||| ||| |||:||: :|||:|
 Db 907 TLFTIFAFVAVAVLMYRRRPEIGGELGGPRGPKIATTCLFFSLWLMYIVFSSLEAYCHVK 966
 Qy 920 GF 921
 ||
 Db 967 GF 968

Search completed: June 24, 2004, 16:14:13
 Job time : 53.0084 secs

OM protein - protein search, using sw model

Run on: June 24, 2004, 15:55:42 ; Search time 17.3323 Seconds
(without alignments)
2766.900 Million cell updates/sec

Title: US-10-054-680-2
Perfect score: 4797
Sequence: 1 MAWLRLQLTSAFLHFGGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4784	99.7	927	1	NAC3_HUMAN	P57103 homo sapien
2	4686	97.7	927	1	NAC3_RAT	P70549 rattus norv
3	3447.5	71.9	970	1	NAC1_CANFA	P23685 canis famil
4	3442.5	71.8	970	1	NAC1_FELCA	P48767 felis silve
5	3439.5	71.7	973	1	NAC1_HUMAN	P32418 homo sapien
6	3432.5	71.6	970	1	NAC1_CAVPO	P48766 cavia porce
7	3428	71.5	971	1	NAC1_RAT	Q01728 rattus norv
8	3425.5	71.4	970	1	NAC1_BOVIN	P48765 bos taurus
9	3405.5	71.0	970	1	NAC1_MOUSE	P70414 mus musculu
10	3373.5	70.3	921	1	NAC2_HUMAN	Q9upr5 homo sapien
11	3357	70.0	921	1	NAC2_RAT	P48768 rattus norv
12	306.5	6.4	1216	1	NKX1_BOVIN	Q28139 bos taurus
13	303.5	6.3	1181	1	NKX1_RAT	Q9qzm6 rattus norv
14	293	6.1	1099	1	NKX1_HUMAN	O60721 homo sapien
15	266	5.5	645	1	NKX3_MOUSE	Q99pd7 mus musculu
16	262.5	5.5	624	1	NKX3_RAT	Q9epq0 rattus norv
17	258.5	5.4	644	1	NKX3_HUMAN	Q9hc58 homo sapien

18	251	5.2	663	1	NKX1_CHICK	Q9ial8	gallus gall
19	247	5.1	605	1	NKX4_HUMAN	Q8nff2	homo sapien
20	246	5.1	605	1	NKX4_MOUSE	Q8cgg8	mus musculu
21	239.5	5.0	661	1	NKX2_HUMAN	Q9ui40	homo sapien
22	231.5	4.8	856	1	NCKX_DROME	Q9u6a0	drosophila
23	227	4.7	670	1	NKX2_RAT	O54701	rattus norv
24	216.5	4.5	651	1	NKX2_CHICK	Q9ial7	gallus gall
25	147	3.1	590	1	YKTA_CAEEL	P34322	caenorhabdi
26	143.5	3.0	325	1	YRBG_ECOLI	P45394	escherichia
27	142.5	3.0	1807	1	ITB4_RAT	Q64632	rattus norv
28	142	3.0	302	1	Y091_METJA	Q57556	methanococc
29	141.5	2.9	572	1	YKT4_CAEEL	P34315	caenorhabdi
30	128.5	2.7	664	1	SYM_BACSU	P37465	bacillus su
31	128.5	2.7	4655	1	LRP2_HUMAN	P98164	homo sapien
32	127	2.6	1822	1	ITB4_HUMAN	P16144	homo sapien
33	125	2.6	700	1	TRDN_CANFA	P82179	canis famil
34	120	2.5	1828	1	MAP2_MOUSE	P20357	mus musculu
35	119.5	2.5	1564	1	MRP2_RABIT	Q28689	oryctolagus
36	119	2.5	673	1	SYM_OCEIH	P59079	oceanobacil
37	118.5	2.5	664	1	SYM_LISMO	Q8yaf2	listeria mo
38	118	2.5	803	1	RIR1_CRYPV	O61065	cryptospori
39	116.5	2.4	664	1	SYM_LISIN	Q92f90	listeria in
40	116	2.4	657	1	SYM_STAAM	Q99wb3	staphylococ
41	116	2.4	657	1	SYM_STAAW	Q8ny00	staphylococ
42	115.5	2.4	1805	1	NEST_RAT	P21263	rattus norv
43	115	2.4	548	1	CH60_EHRSE	O32606	ehrlichia s
44	114	2.4	1036	1	YAN2_SCHPO	Q10068	schizosacch
45	114	2.4	1468	1	RPOB_AQUAE	O67762	aquifex aeo

ALIGNMENTS

RESULT 1

NAC3_HUMAN

ID NAC3_HUMAN STANDARD; PRT; 927 AA.
AC P57103; Q8IUE9; Q8IUFO; Q8NFI7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE 3).
GN SLC8A3 OR NCX3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RX MEDLINE=22294016; PubMed=12406570;
RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
RT "The human SLC8A3 gene and the tissue-specific Na⁺/Ca²⁺ exchanger 3
RT isoforms.";
RL Gene 298:1-7(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=22447378; PubMed=12558991;

RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
 RT "Control of the Na⁺/Ca²⁺ exchanger 3 promoter by cyclic adenosine
 RT monophosphate and Ca²⁺ in differentiating neurons.";
 RL J. Neurochem. 84:282-293(2003).
 RN [3]
 RP SEQUENCE OF 1-595 FROM N.A.
 RA Kraev A.S., Chumakov I.M., Carafoli E.;
 RT "The organization of the human gene of the sodium-calcium exchanger.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores (By similarity).
 CC -!- ENZYME REGULATION: By intracellular calcium ions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=3; Synonyms=NCX3.3;
 CC IsoId=P57103-1; Sequence=Displayed;
 CC Name=2; Synonyms=NCX3.2;
 CC IsoId=P57103-2; Sequence=VSP_008116;
 CC Name=4; Synonyms=NCX3.4;
 CC IsoId=P57103-3; Sequence=VSP_008117, VSP_008118;
 CC -!- TISSUE SPECIFICITY: Isoform 2 is expressed in brain and skeletal
 CC muscle; Isoform 3 is expressed in excitable cells of brain, retina
 CC and skeletal muscle; Isoform 4 is expressed in skeletal muscle.
 CC -----
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 CC -----
 DR EMBL; AF510501; AAN60790.1; -.
 DR EMBL; AF510502; AAN60791.1; -.
 DR EMBL; AF510503; AAN60792.1; -.
 DR EMBL; AF508982; AAM90955.1; -.
 DR EMBL; X93017; -; NOT_ANNOTATED_CDS.
 DR Genew; HGNC:11070; SLC8A3.
 DR MIM; 607991; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 1.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 927 SODIUM/CALCIUM EXCHANGER 3.
 FT DOMAIN 31 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 94 POTENTIAL.
 FT DOMAIN 95 147 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 148 168 POTENTIAL.

FT	DOMAIN	169	169	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	190	POTENTIAL.
FT	DOMAIN	191	202	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	223	POTENTIAL.
FT	DOMAIN	224	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	251	POTENTIAL.
FT	DOMAIN	252	726	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	727	747	POTENTIAL.
FT	DOMAIN	748	754	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	755	775	POTENTIAL.
FT	DOMAIN	776	778	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	779	799	POTENTIAL.
FT	DOMAIN	800	828	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	829	849	POTENTIAL.
FT	DOMAIN	850	860	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	861	881	POTENTIAL.
FT	DOMAIN	882	903	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	927	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	253	272	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	140	180	ALPHA-1.
FT	REPEAT	399	470	BETA-1.
FT	REPEAT	534	604	BETA-2.
FT	REPEAT	796	832	ALPHA-2.
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	823	823	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	630	635	Missing (in isoform 2).
FT				/FTId=VSP_008116.
FT	VARSPPLIC	596	620	KTIRVKIVDEEYERQENFFIALGE -> CDRQEADYGRRG
FT				GQEDSRDGKASIG (in isoform 4).
FT				/FTId=VSP_008117.
FT	VARSPPLIC	621	927	Missing (in isoform 4).
FT				/FTId=VSP_008118.
SQ	SEQUENCE	927 AA;	103009 MW;	7B43CB6A9D77615E CRC64;

Query Match 99.7%; Score 4784; DB 1; Length 927;
 Best Local Similarity 99.4%; Pred. No. 1.5e-300;
 Matches 921; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy	1	MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGVLTVFLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIIETEGDHPKGIEMDGMMNSHFLDGN	300

Db 241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300

Qy 301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR 360
 |||

Db 301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR 360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||

Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDSMTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF 480
 |||

Db 421 KGGDSMTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||

Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600
 |||

Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTEGTAKGGGEDFEDTYGELEFKNDET VKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPV 654
 |||

Db 601 KIVDEEEYERQENFFIALGEPKWMERGISALLSPDVTDRKLTMEEEEAKRIAEMGKPV 660

Qy 655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
 |||

Db 661 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 720

Qy 715 EERLPSCFDYVMHFLTTFWVKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 774
 |||

Db 721 EERLPSCFDYVMHFLTTFWVKVLFACVPPEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 780

Qy 775 CTIGLKDSVTAVVFVAFGTSPDPTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAW 834
 |||

Db 781 CTIGLKDSVTAVVFVAFGTSPDPTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAW 840

Qy 835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
 |||

Db 841 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 900

Qy 895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||

Db 901 TTWLFVSLWLLYILFATLEAYCYIKGF 927

RESULT 2

NAC3_RAT

ID NAC3_RAT STANDARD; PRT; 927 AA.

AC P70549;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
 DE 3).

GN SLC8A3 OR NCX3.

OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=96394663; PubMed=8798769;
 RA Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lysis A.J.,
 RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3."
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By intracellular calcium ions.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expression restricted to brain and skeletal
 CC muscle.
 CC -----
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 CC -----
 DR EMBL; U53420; AAC52817.1; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 927 SODIUM/CALCIUM EXCHANGER 3.
 FT DOMAIN 31 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 94 POTENTIAL.
 FT DOMAIN 95 147 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 148 168 POTENTIAL.
 FT DOMAIN 169 169 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 170 190 POTENTIAL.
 FT DOMAIN 191 202 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 203 223 POTENTIAL.
 FT DOMAIN 224 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 251 POTENTIAL.
 FT DOMAIN 252 726 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 727 747 POTENTIAL.
 FT DOMAIN 748 754 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 755 775 POTENTIAL.
 FT DOMAIN 776 778 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	779	799	POTENTIAL.
FT	DOMAIN	800	828	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	829	849	POTENTIAL.
FT	DOMAIN	850	860	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	861	881	POTENTIAL.
FT	DOMAIN	882	903	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	927	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	253	272	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	140	180	ALPHA-1.
FT	REPEAT	399	470	BETA-1.
FT	REPEAT	534	604	BETA-2.
FT	REPEAT	796	832	ALPHA-2.
FT	DOMAIN	645	648	POLY-GLU.
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	823	823	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	927 AA;	103162 MW;	EAB35F9620DBE69E CRC64;

Query Match 97.7%; Score 4686; DB 1; Length 927;
 Best Local Similarity 96.8%; Pred. No. 3.1e-294;
 Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

Qy	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFG	LVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120	
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120	
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180	
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180	
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240	
Db	181	IIGICVYVIPDGETRRIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQWEGLLTLFF	240	
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300	
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGEHPKGIEMDGKMMNSHFLDGN	300	
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSAFYRIQATR	360	
Db	301	LIPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSAFYRIQATR	360	
Qy	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420	
Db	361	MMTGAGNIIKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR	420	
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480	
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480	
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540	
Db	481	FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540	

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Qy 601 KIVDEEEYERQENFFIALGEPKWMERGIS-----DVTDRKLTMEEEEAKRIAEMGKPVL 654
 |||:|
 Db 601 KIVDEEEYERQENFFIALGEPKWMERGISALLLSPEVTDKLTMEEEEAKRIAEMGKPVL 660

Qy 655 GEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
 |||:|
 Db 661 GEHPKLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDESG 720

Qy 715 EERLPSCFDYVMHFLTTFVWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFG 774
 |||
 Db 721 EERLPSCFDYVMHFLTTFVWKVLFACVPPTTEYCHGWACFVVSILIIIGMLTAIIGDLASHFG 780

Qy 775 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAW 834
 |||
 Db 781 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAW 840

Qy 835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
 |||:|
 Db 841 SVAAIYWAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLA 900

Qy 895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
 |||:|
 Db 901 TTWLFVSLWLLYVLFATLEAYCYIKGF 927

RESULT 3

NAC1_CANFA

ID NAC1_CANFA STANDARD; PRT; 970 AA.
 AC P23685;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=91047958; PubMed=1700476;
 RA Nicoll D.A., Longoni S., Philipson K.D.;
 RT "Molecular cloning and functional expression of the cardiac
 RT sarcolemmal Na(+)-Ca2+ exchanger.";
 RL Science 250:562-565(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92152737; PubMed=1785844;
 RA Nicoll D.A., Philipson K.D.;

```

RT  "Molecular studies of the cardiac sarcolemmal sodium-calcium
RT  exchanger.";
RL  Ann. N.Y. Acad. Sci. 639:181-188(1991).
CC  -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC  coupling. Ca(2+) is extruded from the cell during relaxation so as
CC  to prevent overloading of intracellular stores.
CC  -!- ENZYME REGULATION: By ATP.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC  -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC  -----
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CC  -----
DR  EMBL; M57523; AAA62766.1; -.
DR  PIR; A36417; A36417.
DR  InterPro; IPR003644; Calx_beta.
DR  InterPro; IPR004836; Na_Ca_Ex.
DR  InterPro; IPR004837; NaCa_Exmemb.
DR  Pfam; PF03160; Calx-beta; 2.
DR  Pfam; PF01699; Na_Ca_Ex; 2.
DR  PRINTS; PR01259; NACAEXCHNGR.
DR  SMART; SM00237; Calx_beta; 2.
DR  TIGRFAMs; TIGR00845; caca; 1.
KW  Transport; Antiport; Calcium transport; Sodium transport;
KW  Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW  Calmodulin-binding; Repeat.
FT  SIGNAL      1      32      POTENTIAL.
FT  CHAIN       33     970     SODIUM/CALCIUM EXCHANGER 1.
FT  DOMAIN      33      71     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    72      93     POTENTIAL.
FT  DOMAIN      94     133     CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM   134     155     POTENTIAL.
FT  DOMAIN     156     167     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM   168     188     POTENTIAL.
FT  DOMAIN     189     199     CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM   200     222     POTENTIAL.
FT  DOMAIN     223     225     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM   226     249     POTENTIAL.
FT  DOMAIN     250     769     CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM   770     789     POTENTIAL.
FT  DOMAIN     790     796     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM   797     819     POTENTIAL.
FT  DOMAIN     820     821     CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM   822     840     POTENTIAL.
FT  DOMAIN     841     871     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM   872     892     POTENTIAL.
FT  DOMAIN     893     903     CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM   904     924     POTENTIAL.
FT  DOMAIN     925     941     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM   942     958     POTENTIAL.
FT  DOMAIN     959     970     CYTOPLASMIC (POTENTIAL).
FT  DOMAIN     251     270     CALMODULIN-BINDING (POTENTIAL).

```

FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108004 MW;	BBDBCC584846AE08 CRC64;

Query Match 71.9%; Score 3447.5; DB 1; Length 970;
 Best Local Similarity 69.2%; Pred. No. 2.3e-214;
 Matches 677; Conservative 109; Mismatches 127; Indels 65; Gaps 10;

Qy	1	MAWLRQLPLTSAFLHFGVLTFVLF--LNLRAEAGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : :	
Db	1	MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPN	118
		: :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFGLGVSIIDRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
		: :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: :	
Db	177	FIIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKG---IEMDGKMMNSH	295
		: : : :	
Db	237	FFFPICVVFVAVADRLLLFYKYVYKRYRAGKQRMIIIEHEDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQVEMANYALSHQQ	348
Db	297	VDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
		: : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYYQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : :	
Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qy	468	IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
		: : :	
Db	476	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592

Qy	588	EFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERG-----	627
		: :: : : : : : : :	
Db	593	EFQNDEIVKTISVKVIDDEEYEKNKTF FLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEPKLEVI	663
		: : : : :	
Db	653	YGQPVFRKVHAREHPI PSTVITIAEEYDDKQPLTSKEEEEERRIAEMGRPILGEHTKLEVI	712
Qy	664	IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD	723
		: : : : :	
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTSNWSREQFIEAITVSAGEDDDDDDECGEKLPSCFD	772
Qy	724	YVMHFLT VFWKVLFA CVPPTEYCHGWACFAVSILII GMLTAII GDLASHFGCTIGLKDSV	783
		: :	
Db	773	YVMHFLT VFWKVLFAFVPPTEYWNGWACFIVSILMIGILTAFIGDLASHFGCTIGLKDSV	832
Qy	784	TAVVFVAFGTSVPD TFASKAAALQDVYADASIGNVTGSNAVN VFLGIGLAWSVA AIYWAL	843
		: :	
Db	833	TAVVFVALGTSVPD TFASKVAATQDQYADASIGNVTGSNAVN VFLGIGVAWSIA AIYHAA	892
Qy	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW	903
		: : : : : :	
Db	893	NGEQFKVSPGTLAFSVTLFTIFAFINVG VLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW	952
Qy	904	LLYILFATLEAYCYIKGF	921
		: :	
Db	953	LLYIFFSSLEAYCHIKGF	970

RL J. Biol. Chem. 272:11510-11517(1997).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; L35846; AAB41941.1; -.
 DR EMBL; U67075; AAB40148.1; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 822 840 POTENTIAL.
 FT DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 872 892 POTENTIAL.
 FT DOMAIN 893 903 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 904 924 POTENTIAL.
 FT DOMAIN 925 941 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 942 958 POTENTIAL.
 FT DOMAIN 959 970 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 251 270 CALMODULIN-BINDING (POTENTIAL).
 FT REPEAT 138 178 ALPHA-1.
 FT REPEAT 407 478 BETA-1.

FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	21	21	P -> A (IN REF. 2).
FT	CONFLICT	113	113	K -> N (IN REF. 2).
SQ	SEQUENCE	970 AA;	108004 MW;	2402F02DE35D4057 CRC64;

Query Match 71.8%; Score 3442.5; DB 1; Length 970;
 Best Local Similarity 69.3%; Pred. No. 4.9e-214;
 Matches 678; Conservative 108; Mismatches 126; Indels 67; Gaps 12;

Qy	1	MAWLRLQPLTSAFLHFLVTFV-LFLNGLRAEAGGSGDVPSTGQNNES--CSGSSDCKEG	57
		: : : :	
Db	1	MLRLRLSPTFSVGFH--LLAFVPLLFSHVDLI---SADTEMEGEGNETGECTGSYYCKKG	55
Qy	58	VILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKP	117
		:	
Db	56	VILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKP	115
Qy	118	NGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFN	177
		: :	
Db	116	NGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFN	175
Qy	178	MFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLT	237
		: :	
Db	176	MFIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLT	235
Qy	238	LFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNS	294
		: :	
Db	236	FFFFPICVVFVAVADRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVVNS	295
Qy	295	H---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQ	347
		:	
Db	296	HVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQ	354
Qy	348	QKSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQ	406
		:	
Db	355	QKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQYQ	414
Qy	407	CLENCGAVLLTVVRKGGDMSTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSV	466
		:	
Db	415	CLENCGTVALTILRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRV	474
Qy	467	GIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDD	526
		: : :	
Db	475	GIIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDD	531
Qy	527	DHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGE	586
		:	
Db	532	DHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGE	591
Qy	587	LEFKNDETVKTIRVKIVDEEYERQENFFIALGEPKWMERG-----	627

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      |||:| | | | | | | | | | | | : | | : | | : |
Db      592 LEFQND EIVK TISVKVIDDEEYEKNTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKY 651
Qy      628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEPKLEV 662
      | : | | | | : | | | | | | | | | | | | | |
Db      652 LYGQPVFRKVVHAREHPISTVITIAEECDAKQPLTSKEEEERRIAEMGRPILGEHTKLEV 711
Qy      663 IIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCF 722
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      712 IIEESYEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDDECGEELPSCF 771
Qy      723 DYVMHFLT VFWKVL FACVPPEYCHGWACFAVSILIIGMTAIIGDLASHFGCTIGLKDS 782
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      772 DYVMHFLT VFWKVL FAFVPPEYWNGWACFIVSILMIGILTAFIGDLASHFGCTIGLKDS 831
Qy      783 VTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWA 842
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      832 VTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVLGIGVAWSIAAIYHA 891
Qy      843 LQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSL 902
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      892 ANGEQFKVSPGTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSCLFVLL 951
Qy      903 WLLYILFATLEAYCYIKGF 921
      | | | | | | : | | | | | | | |
Db      952 WLLYIFFSSLEAYCHIKGF 970

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RESULT 5

NAC1_HUMAN

```

ID      NAC1_HUMAN      STANDARD;      PRT;      973 AA.
AC      P32418; Q95849; Q9UBL8; Q9UDN1; Q9UDN2; Q9UKX6;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE      1).
GN      SLC8A1 OR NCX1 OR CNC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Heart;
RX      MEDLINE=92262521; PubMed=1374913;
RA      Komuro I., Wenninger K.E., Philipson K.D., Izumo S.;
RT      "Molecular cloning and characterization of the human cardiac Na+/Ca2+
RT      exchanger cDNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).
RX      MEDLINE=21136211; PubMed=11241183;
RA      Van Eylen F., Bollen A., Herchuelz A.;
RT      "NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.";
RL      J. Endocrinol. 168:517-526(2001).
RN      [3]

```

RP SEQUENCE FROM N.A. (ISOFORM 7).
 RA Mangini N.J., Chen W., Wang Q., Kennedy B.G.;
 RT "Na+/Ca2+ exchanger isoforms in cultured human retinal pigment
 epithelium.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 1-603 FROM N.A.
 RA Rohlfing T., Strowmatt C., Scronce D., Moody T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 850-973 FROM N.A.
 RA Kozlowicz A., Stoneking T., Hawkins M., Le T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).
 RA Lundquist P., Lundgren T., Gritli-Linde A., Linde A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 coupling. Ca(2+) is extruded from the cell during relaxation so as
 to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=NaCa1, NCX1.1;
 CC IsoId=P32418-1; Sequence=Displayed;
 CC Name=3; Synonyms=NaCa3, NCX1.3;
 CC IsoId=P32418-2; Sequence=VSP_003397, VSP_003398, VSP_003400;
 CC Name=7; Synonyms=NaCa7, NCX1.7;
 CC IsoId=P32418-3; Sequence=VSP_003397, VSP_003398, VSP_003399;
 CC Name=10; Synonyms=NaCa10, NCX1.10;
 CC IsoId=P32418-4; Sequence=VSP_003397, VSP_003398;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 DR EMBL; M91368; AAA35702.1; -.
 DR EMBL; AF108388; AAF08987.1; -.
 DR EMBL; AF108389; AAF08988.1; -.
 DR EMBL; AF128524; AAD26362.1; -.
 DR EMBL; AC007281; AAF19237.1; -.
 DR EMBL; AC007254; AAF19235.1; -.
 DR EMBL; AF115505; AAD17213.1; -.
 DR PIR; S32815; S32815.
 DR Genew; HGNC:11068; SLC8A1.
 DR MIM; 182305; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015085; F:calcium ion transporter activity; TAS.
 DR GO; GO:0015081; F:sodium ion transporter activity; TAS.
 DR GO; GO:0006816; P:calcium ion transport; TAS.

DR GO; GO:0006936; P:muscle contraction; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing; Polymorphism.
 FT SIGNAL 1 35 POTENTIAL.
 FT CHAIN 36 973 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 36 74 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 75 96 POTENTIAL.
 FT DOMAIN 97 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 158 POTENTIAL.
 FT DOMAIN 159 170 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 202 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 203 225 POTENTIAL.
 FT DOMAIN 226 228 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 229 252 POTENTIAL.
 FT DOMAIN 253 772 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 773 792 POTENTIAL.
 FT DOMAIN 793 799 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 800 822 POTENTIAL.
 FT DOMAIN 823 824 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 825 843 POTENTIAL.
 FT DOMAIN 844 874 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 875 895 POTENTIAL.
 FT DOMAIN 896 906 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 907 927 POTENTIAL.
 FT DOMAIN 928 944 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 945 961 POTENTIAL.
 FT DOMAIN 962 973 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 254 273 CALMODULIN-BINDING (POTENTIAL).
 FT REPEAT 141 181 ALPHA-1.
 FT REPEAT 410 481 BETA-1.
 FT REPEAT 542 612 BETA-2.
 FT REPEAT 842 878 ALPHA-2.
 FT DOMAIN 239 242 POLY-PHE.
 FT DOMAIN 692 695 POLY-GLU.
 FT DOMAIN 759 763 POLY-ASP.
 FT MOD_RES 392 392 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 869 869 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 605 613 TISVKVIDD -> IITIRIFDR (in isoform 3,
 FT isoform 7 and isoform 10).
 FT /FTId=VSP_003397.
 FT VARSPLIC 619 645 NKTFLEIGEPRLVEMSEKKALLLNEL -> ECSFSLVLEE
 FT PKWIRRGMK (in isoform 3, isoform 7 and
 FT isoform 10).
 FT /FTId=VSP_003398.

FT VARSPLIC 652 656 Missing (in isoform 7).
 FT /FTId=VSP_003399.
 FT VARSPLIC 652 679 Missing (in isoform 3).
 FT /FTId=VSP_003400.
 FT VARIANT 692 692 E -> V (in dbSNP:5557).
 FT /FTId=VAR_014847.
 SQ SEQUENCE 973 AA; 108546 MW; 17DFC1B1F15921D8 CRC64;

Query Match 71.7%; Score 3439.5; DB 1; Length 973;
 Best Local Similarity 68.9%; Pred. No. 7.7e-214;
 Matches 674; Conservative 111; Mismatches 128; Indels 65; Gaps 10;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLGRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : : : : :	
Db	4	MRRLSLSPTFSMGFHLLVTVSLLFSHVDHVIAETEMEGEGNETGE---CTGSYYCKKGV	59
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIKKPN	118
		: : : : : : : :	
Db	60	ILPIWEPQDPSPFGDKIARATVYFVAMVYMFLGVSIADRFRMSIEVITSQEKEITIKKPN	119
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
		: : :	
Db	120	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	179
Qy	179	FIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLMIYLAVFSPGVVQVWEGLLTL	238
		: : : : : : : :	
Db	180	FIIIALCVYVVPDGETRGIKHLRVFFVTAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	239
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : : :	
Db	240	FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHEDRPSSKTEIEMDGKVVNSH	299
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
		: : : : : : : : :	
Db	300	VENFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ	358
Qy	349	KSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQC	407
		: : : : : : : : : : : :	
Db	359	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSКИFFEQGTQC	418
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : : : : : : : : :	
Db	419	LENCGTVALTIIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKEPGDTQKEIRVG	478
Qy	468	IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
		: : : : :	
Db	479	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD	535
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
		: : : : : :	
Db	536	HAGIFTFEPPVTHVSESIGIMEVKVLRITSGARGNVIVPYKTIEGTARGGGGEDFEDTCGEL	595
Qy	588	EFKNDETVKTIRVKIVDEEYERQENFFIALGEPKWMERG-----	627
		: : : : : : : : : :	
Db	596	EFQNDIVKTIISVKVIDDEEYEKNKTFEIGEPRLVEMSEKKALLLNELGGFTITGKYL	655
Qy	628	-----ISDVTDRK---LTMEEEEAKRIAEMGKPVLGHPKLEVI	663

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DR EMBL; U04955; AAA73904.1; -.
 DR PIR; I48097; I48097.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 822 840 POTENTIAL.
 FT DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 872 892 POTENTIAL.
 FT DOMAIN 893 903 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 904 924 POTENTIAL.
 FT DOMAIN 925 941 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 942 958 POTENTIAL.
 FT DOMAIN 959 970 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 251 270 CALMODULIN-BINDING (POTENTIAL).
 FT REPEAT 138 178 ALPHA-1.
 FT REPEAT 407 478 BETA-1.
 FT REPEAT 539 609 BETA-2.
 FT REPEAT 839 875 ALPHA-2.
 FT DOMAIN 236 239 POLY-PHE.
 FT DOMAIN 689 692 POLY-GLU.
 FT DOMAIN 756 760 POLY-ASP.
 FT MOD_RES 389 389 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 970 AA; 108071 MW; 72D364CB8D157739 CRC64;

Query Match 71.6%; Score 3432.5; DB 1; Length 970;

Db	773	YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSV	832
Qy	784	TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWAL	843
		: :	
Db	833	TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVLGIGVAWSIAAIYHAA	892
Qy	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFLVSLW	903
		: : : : :	
Db	893	NGEQFKVSPGTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSCFLVLLW	952
Qy	904	LLYILFATLEAYCYIKGF	921
		: :	
Db	953	LLYIFFSSLEAYCHIKGF	970

RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3.";
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Heart, NaCa1;
 CC IsoId=Q01728-1; Sequence=Displayed;
 CC Name=2; Synonyms=Brain-1, NaCa5;
 CC IsoId=Q01728-2; Sequence=VSP_003402, VSP_003403;
 CC Name=3; Synonyms=Brain-2, NaCa4;
 CC IsoId=Q01728-3; Sequence=VSP_003402, VSP_003404;
 CC Name=4; Synonyms=Kidney-1, NaCa7;
 CC IsoId=Q01728-4; Sequence=VSP_003401, VSP_003402, VSP_003403;
 CC Name=5; Synonyms=Kidney-2, NaCa3;
 CC IsoId=Q01728-5; Sequence=VSP_003401, VSP_003402, VSP_003404;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma or brain, and spleen.

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 CC -----

DR EMBL; X68191; CAA48273.1; -.
 DR EMBL; X68812; CAA48707.1; -.
 DR EMBL; X68813; CAA48708.1; -.
 DR EMBL; U04933; AAB39952.1; -.
 DR EMBL; U04934; AAA19124.1; -.
 DR EMBL; U04936; AAA19125.1; -.
 DR PIR; A53789; A53789.
 DR PIR; S28833; S28833.
 DR PIR; S32435; S32435.
 DR PIR; S43730; S43730.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 971 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.

FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	770	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	771	790	POTENTIAL.
FT	DOMAIN	791	797	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	798	820	POTENTIAL.
FT	DOMAIN	821	822	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	823	841	POTENTIAL.
FT	DOMAIN	842	872	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	873	893	POTENTIAL.
FT	DOMAIN	894	904	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	905	925	POTENTIAL.
FT	DOMAIN	926	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	943	959	POTENTIAL.
FT	DOMAIN	960	971	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	840	876	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	690	693	POLY-GLU.
FT	DOMAIN	757	761	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (BY SIMILARITY).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	867	867	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	602	635	TISVKVIDDEEYEKNTFFIEIGEPRLVEMSEKK -> IIT
FT				IRIFDREEYEKCSFSLVLEEPKWIRRGMK (in
FT				isoform 4 and isoform 5).
FT				/FTId=VSP_003401.
FT	VARSPPLIC	636	642	Missing (in isoform 2, isoform 3, isoform
FT				4 and isoform 5).
FT				/FTId=VSP_003402.
FT	VARSPPLIC	649	654	Missing (in isoform 2 and isoform 4).
FT				/FTId=VSP_003403.
FT	VARSPPLIC	649	677	Missing (in isoform 3 and isoform 5).
FT				/FTId=VSP_003404.
FT	CONFLICT	250	250	D -> A (IN REF. 1).
FT	CONFLICT	402	402	P -> A (IN REF. 1).
SQ	SEQUENCE	971 AA;	108184 MW;	EC456CFE3AFC6A69 CRC64;

Query Match 71.5%; Score 3428; DB 1; Length 971;
 Best Local Similarity 68.7%; Pred. No. 4.2e-213;
 Matches 675; Conservative 106; Mismatches 124; Indels 78; Gaps 11;

Qy	4	LRLQPLTSAFLHFGVLTVFLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRVLTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: : : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113

Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAA	175
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEG	235
Db	174	FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEG	233
Qy	236	LTFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKG---IEMDGKMM	292
Db	234	LTFFFFPICVVFVAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
Db	294	NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	HQQKSRAFYRIQATRLMTAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	412
Qy	405	YQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLNCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRSSEVSEDG---ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTIVHSESIGIMEVKVLRRTSGARGNVIIIPYKTIEGTARGGGEDFEDT	588
Qy	584	YGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMER-----	626
Db	589	CGELEFQND EIVKTI SVKVIDDEEYKNTFFIEIGEPRLVEMSEKKALLLNELGGFTLT	648
Qy	627	-----GISDVTDRK--LTMEEEEAKRIAEMGKPVLGHP	658
Db	649	EGKKMYGQPVFRKVHARDHPISTVISISEEYDDKQPLTSKEEEEERRIAEMGRPILGEHT	708
Qy	659	KLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERL	718
Db	709	KLEVIIIEESYEFKSTVDKLIKKTNLALVVGTHSWRQFIEAITVSAGEDDDDDDECGEERL	768
Qy	719	PSCFDYVMHFLT VFWKVLFAVPPTEYCHGWACFAVSILIIIGMLTAIGDLASHFGCTIG	778
Db	769	PSCFDYVMHFLT VFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIG	828
Qy	779	LKDSVTAVVFAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAA	838
Db	829	LKDSVTAVVFAFGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGLAWSVAA	888
Qy	839	IYWALQGGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTTWL	898
Db	889	IYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLVYRRRPEIGELGGPRGCKLATTTWL	948

Qy 899 FVSLWLLYILFATLEAYCYIKGF 921
 || ||||| |:||||:||||
 Db 949 FVLLWLLYIFFSSLEAYCHIKGF 971

RESULT 8

NAC1_BOVIN

ID NAC1_BOVIN STANDARD; PRT; 970 AA.
 AC P48765;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=93037494; PubMed=1416984;
 RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
 RA Nicoll D.A., Philipson K.D., Reeves J.P.;
 RT "Cloning and expression of the bovine cardiac sodium-calcium
 RT exchanger.";
 RL Arch. Biochem. Biophys. 298:553-560(1992).
 RN [2]
 RP SUBCELLULAR LOCATION.
 RC TISSUE=Retinal rod cell;
 RX MEDLINE=90241959; PubMed=2334719;
 RA Reid D.M., Friedel U., Molday R.S., Cook N.J.;
 RT "Identification of the sodium-calcium exchanger as the major
 RT ricin-binding glycoprotein of bovine rod outer segments and its
 RT localization to the plasma membrane.";
 RL Biochemistry 29:1601-1607(1990).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; L06438; AAA30509.1; -.
 DR PIR; S27114; S27114.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.

Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFSMSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
Db	237	FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQVLVEMANYALSHQQ	348
Db	297	VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	356	KSRAFYRIQATRLMTAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYYQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	416	LENCGTVALTIIRGGDLTNTVFDFTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qy	468	IIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	476	IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEPPVTHVSESIGIMEVKVLRITSGARGNVIVPYKTIEGTARGGGGEDFEDTCGEL	592
Qy	588	EFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERG-----	627
Db	593	EFQND EIVKTI SVKVIDDEEYKNTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qy	628	-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGHPKLEVI	663
Db	653	YGQPVFRKVHAREHPLPSTIITIAD EYDDKQPLTSKEEEEERRIAEMGRPILGEHTRLEVI	712
Qy	664	IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD	723
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDDECGEKLPSCFD	772
Qy	724	YVMHFLT VFWKVLFAVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSV	783
Db	773	YVMHFLT VFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV	832
Qy	784	TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL	843
Db	833	TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA	892
Qy	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGELGGPRGCKLATTWLFVSLW	903

Db 893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLlyRRRPEIGGELGGPRTAKLLTSCLFVLLW 952

Qy 904 LLYILFATLEAYCYIKGF 921
 |||| |::|||||:||||

Db 953 LLYIFFSSLEAYCHIKGF 970

RESULT 9

NAC1_MOUSE

ID NAC1_MOUSE STANDARD; PRT; 970 AA.

AC P70414;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

DE 1).

GN SLC8A1 OR NCX.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RX MEDLINE=96250070; PubMed=8659820;

RA Kim I., Lee C.O.;

RT "Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional expression in Xenopus oocytes.";

RL Ann. N.Y. Acad. Sci. 779:126-128(1996).

CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction coupling. Ca(2+) is extruded from the cell during relaxation so as to prevent overloading of intracellular stores.

CC -!- ENZYME REGULATION: By ATP.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.

CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.

CC -----

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CC -----

DR EMBL; U70033; AAB46708.1; -.

DR MGD; MGI:107956; Slc8a1.

DR InterPro; IPR003644; Calx_beta.

DR InterPro; IPR004836; Na_Ca_Ex.

DR InterPro; IPR004837; NaCa_Exmemb.

DR Pfam; PF03160; Calx-beta; 2.

DR Pfam; PF01699; Na_Ca_Ex; 2.

DR PRINTS; PR01259; NACAEXCHNGR.

DR SMART; SM00237; Calx_beta; 2.

DR TIGRFAMs; TIGR00845; caca; 1.

KW Transport; Antiport; Calcium transport; Sodium transport;

KW Transmembrane; Glycoprotein; Phosphorylation; Signal;

KW Calmodulin-binding; Repeat.

FT	SIGNAL	1	32	POTENTIAL.
FT	CHAIN	33	970	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	155	POTENTIAL.
FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	769	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	770	789	POTENTIAL.
FT	DOMAIN	790	796	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	820	821	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA; 108035 MW; F5FC0BD07F2B6602 CRC64;		

Query Match 71.0%; Score 3405.5; DB 1; Length 970;
 Best Local Similarity 68.3%; Pred. No. 1.2e-211;
 Matches 665; Conservative 111; Mismatches 138; Indels 59; Gaps 8;

Qy	4	LRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIW	63
		: : : : : :	
Db	2	LRLSLPPNVSMGFRLVALVALLFSHVDHITADTEAETGGNETTECTGSYYCKKGVILPIW	61
Qy	64	YPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST	123
		:: ::: : : : :	
Db	62	EPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTK	121
Qy	124	TTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMFIIG	183
		: : : : :	
Db	122	TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIA	181
Qy	184	ICVYVIPDGETRTRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPV	243
		: : : : : : : :	

Db 182 LCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEWEGLLTFFFFPI 241

Qy 244 CVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FL 297
 ||: ||||:||||||:|:| | ||:| | | | ||||:| | | ||

Db 242 CVVFAWVADRLLFYKYVYKRYRAGKQGRMIIIEHEGDRPASKTEIEMDGKVVNSHVDNFL 301

Qy 298 DGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQOKSRAF 353
 || || | | | | :||| |||:||||||:|:|:| | | | |||||

Db 302 DGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAF 360

Qy 354 YRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCG 412
 |||||:||||||:|:|:| | | | : : | | :|:| | :|||

Db 361 YRIQATRLMTGAGNILLKRAADQARKAVSMHEVNMEMAENDPVSKIFFEQGTQCLENCG 420

Qy 413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDD 472
 | ||:|:|:| | | :|:|:|:|:| | | :||| |||: | ||||| | |||||

Db 421 TVALTIMRRGGDLSTTVFVDFRTEDGTANAASDYEFTEGTVIFKPGETQKEIRVGIIDDD 480

Qy 473 IFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF 532
 |||||:| | ||||: : |:| : : : | | | | |:| | |||||

Db 481 IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATITIFDDDHAGIF 537

Qy 533 TFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTEGTAKGGGEDFEDTYGELEFKND 592
 ||| |||||:| ||||| ||||| |||:|:|:|:|:| ||||| || ||:| |

Db 538 TFEEPVTHVSESIGIMEVKVLRTSGARGNVIIIPYKTIEGTARGGGEDFEDTCGEPEFQND 597

Qy 593 ETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG----- 627
 | ||| ||:|:|:|:| : ||| :|:| : |

Db 598 EIVKTISVKVIDDEEYKNTFFIEIGEPRLVEMSEKKALLLNELGGFTLTGKEMYGQPI 657

Qy 628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEPKLEVIIIEESY 668
 ||: | | | | :| | :|||:|:| | ||||:| |

Db 658 FRKVHARDHPISTVITISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIQESY 717

Qy 669 EFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHF 728
 ||:||||||| |||||:|:|:| ||||| |:|:| ||:|||||||

Db 718 EFKSTVDKLIKKTNLALVVGTSWREQFIEAITVSAGEDDDDDDECGEKLPSCFDYVMHF 777

Qy 729 LTVFWKVLFAFVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788
 ||||| ||||| :||| ||||:|:| | ||||| ||||| ||||| |||||

Db 778 LTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVF 837

Qy 789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEF 848
 || ||||| || | | ||||| |||||:|:|:| | | :|

Db 838 VALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVLGIGVAWSIAAIYHAANGEQF 897

Qy 849 HVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL 908
 || ||||| |||||: : ||||| :||| || | : || |||||

Db 898 KVSPGTLAFSVTLFTIFAFINVGVLRYRRRPEIGGELGGPRTAKLTLSSLFVLLWLLYIF 957

Qy 909 FATLEAYCYIKGF 921
 |:| ||||:| | |

Db 958 FSSLEAYCHIKGF 970

ID NAC2_HUMAN STANDARD; PRT; 921 AA.
 AC Q9UPR5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
 DE 2).
 GN SLC8A2 OR NCX2 OR KIAA1087.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:197-205(1999).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores (By similarity).
 CC -!- ENZYME REGULATION: By ATP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -----
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 CC -----
 DR EMBL; AB029010; BAA83039.1; ALT_INIT.
 DR Genew; HGNC:11069; SLC8A2.
 DR MIM; 601901; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 921 SODIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 21 68 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 69 90 POTENTIAL.
 FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 152 POTENTIAL.
 FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	165	185	POTENTIAL.
FT	DOMAIN	186	196	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	197	219	POTENTIAL.
FT	DOMAIN	220	222	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	223	246	POTENTIAL.
FT	DOMAIN	247	720	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	721	740	POTENTIAL.
FT	DOMAIN	741	747	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	748	770	POTENTIAL.
FT	DOMAIN	771	772	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	773	791	POTENTIAL.
FT	DOMAIN	792	822	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	823	843	POTENTIAL.
FT	DOMAIN	844	854	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	855	875	POTENTIAL.
FT	DOMAIN	876	892	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	893	909	POTENTIAL.
FT	DOMAIN	910	921	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	248	267	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	135	175	ALPHA-1.
FT	REPEAT	397	468	BETA-1.
FT	REPEAT	527	597	BETA-2.
FT	REPEAT	790	826	ALPHA-2.
FT	DOMAIN	29	32	POLY-PRO.
FT	DOMAIN	638	641	POLY-GLU.
FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	817	817	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	921 AA;	100367 MW;	798CDF7E32B9410C CRC64;

Query Match 70.3%; Score 3373.5; DB 1; Length 921;
Best Local Similarity 71.0%; Pred. No. 1.3e-209;
Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;

Qy	395	ISKVFEDPCSYQCLENCAGVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVV	454
Db	393	ASRIFFEPSLYHCLENCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDY EYSEGLTV	452
Qy	455	LKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR	510
Db	453	FKPGETQKELRIGIIDDDIFEEDHFFVRLNLRVGDAQGMFEPDGG-----GRPK	503
Qy	511	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE	570
Db	504	GRLVAPLLATVTILDDDHAGIFS FQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD	563
Qy	571	GTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWMERGISD	630
Db	564	GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEY EKKNDFFIELGQPQWLKRGISA	623
Qy	631	VT-----DRKLTMEEEEEAKRIAEMGKPV LGEHPKLEVIIEESYEFKTTVDKLIKKTNLA	684
Db	624	LLNQGDGDRKLTAE EEEEARRIAEMGKPV LGENCRLEVIIEESYDFKNTVDKLIKKTNLA	683
Qy	685	LVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHFLT VFWKVLFACVPP	742
Db	684	LVIGTHSWREQFLEAITVS-AGDEEE EEDGSREERLPSCFDYVMHFLT VFWKVLFACVPP	742
Qy	743	TEYCHGWACFAVSILII GMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK	802
Db	743	TEYCHGWACFGVSILVIGLLTALIGDLASHFGCTVGLKDSVNAVVFVALGTSIPDTFASK	802
Qy	803	AAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF	862
Db	803	VAALQDQCADASIGNVTGSNAVNVFLGLGVAVSVAAVYWAVQGRPFVVRTGT LAFSVTLF	862
Qy	863	TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF	921
Db	863	TVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWLLYILFASLEAYCHIRGF	921

RT "Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca2+
 RT exchanger.";
 RL J. Biol. Chem. 269:17434-17439(1994).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96394663; PubMed=8798769;
 RA Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusi A.J.,
 RA Philipson K.D.;
 RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain and skeletal muscle.
 CC -----
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 CC -----
 DR EMBL; U08141; AAA19920.1; -.
 DR PIR; A54139; A54139.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 921 SODIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 21 68 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 69 90 POTENTIAL.
 FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 152 POTENTIAL.
 FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 165 185 POTENTIAL.
 FT DOMAIN 186 196 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 197 219 POTENTIAL.
 FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 223 246 POTENTIAL.
 FT DOMAIN 247 720 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 721 740 POTENTIAL.
 FT DOMAIN 741 747 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 748 770 POTENTIAL.
 FT DOMAIN 771 772 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 773 791 POTENTIAL.

FT	DOMAIN	792	822	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	823	843	POTENTIAL.
FT	DOMAIN	844	854	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	855	875	POTENTIAL.
FT	DOMAIN	876	892	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	893	909	POTENTIAL.
FT	DOMAIN	910	921	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	248	267	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	135	175	ALPHA-1.
FT	REPEAT	397	468	BETA-1.
FT	REPEAT	527	597	BETA-2.
FT	REPEAT	790	826	ALPHA-2.
FT	DOMAIN	29	32	POLY-PRO.
FT	DOMAIN	638	641	POLY-GLU.
FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	817	817	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	921 AA;	100522 MW;	0CDB26BEACBCF6B1 CRC64;

Query Match 70.0%; Score 3357; DB 1; Length 921;

Best Local Similarity 69.6%; Pred. No. 1.5e-208;

Matches 635; Conservative 130; Mismatches 114; Indels 34; Gaps 9;

Qy	31	EAGGSGDVPSTGQNN-----SCSGSSDCKEGVILPIWYPENPSLGDKRIARVIVYFVALI	85
		: : : : : : : : : : :	
Db	21	EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMV	80
Qy	86	YMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA	145
		: : : : : : : :	
Db	81	YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA	140
Qy	146	PEILLSLIEVCCHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFI	205
		: : : : : : : : :	
Db	141	PEILLSVIEVCCHNFQAGELGPGTIVGSAAFNMFVVIACVYVIPAGESRKIKHLRVFFV	200
Qy	206	TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY	265
		: : : : : : : : : : : : : : : :	
Db	201	TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFPVCVVFAMMADKRLLFYKYVYKRY	260
Qy	266	RTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRIL	320
		: : : : : : : :	
Db	261	RTDPRSGIIIGAEGDPPKSIELDGTFGVTE-VPGELGALGTGPAEARELDASRREVIQIL	319
Qy	321	KDLKQKHPEKDLDQLVEMANYALSHQOKSRAFYRIQATRMGTAGNILKKHAAEQAKKA	380
		: : : : : : : : : : : : : :	
Db	320	KDLKQKHDPKDLEQLVGIKYYALLHQOKSRAFYRIQATRLMTGAGNVLRRHAADAARRP	379
Qy	381	SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSA	440
		: : : : : : : : : : : : : : :	
Db	380	GA-NDGAPDDEDDGASRIFFEPSLYHCLENCGSVLLSVACQGGEGNSTFYVDYRTEDGSA	438
Qy	441	NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQ----PEE	496
		: : : : : : : : : : : : : : : : :	
Db	439	KAGSDYEYSEGLVFKPGETQKELRIGIIDDDIFEDEHFFVRLNLRVGDAQGMFEPDG	498
Qy	497	GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRSTS	556
		: : : : : : : : : : : : : : : : : : :	
Db	499	G-----GRPKGRLVAPLLATVTILDDDHAGIFSQDRLLHVSECMGTVDVRVVRSS	549

Qy 557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIIRVKIVDEEEYERQENFFI 616
 ||||| :|:|:|:|:|:| :| | ||| :|:|:|:|:|:|:|:|:|:|:|:|
 Db 550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYKKNFFI 609

Qy 617 ALGEPKWMERGISDVT-----DRKLTMEEEEAARIAEMGKPVLGEPKLEVIIIEESYEF 670
 ||:|:|:|:|:| : |||| | ||||:|:|:|:|:|:|:|:|:|:|:|:|
 Db 610 ELGQPQWLKRGISALLLNQGDGDRKLTAEEEEAQRIAEMGKPVLGENCRLVIIIEESYDF 669

Qy 671 KTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHF 728
 | |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 670 KNTVDKLIKKTNLALVIGTHSWREQFLEAVTVS-AGDEEDEDGDSREERLPSCFDYVMHF 728

Qy 729 LTVFWKVLFACVPPTTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788
 |||||:|:|:|:|:|:| | ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 729 LTVFWKVLFACLPPTTEYCHGWACFGVCILVIGLLTALIGDLASHFGCTVGLKDSVNAVVF 788

Qy 789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEF 848
 || ||:|:|:|:|:| |||| | |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 789 VALGTSIPDTFASKVAALQDQCADASIGNVTGSNAVNVLGLGVAWSVAAVYWAVQGRPF 848

Qy 849 HVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL 908
 | |||||:|:|:|:|:|:| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 849 EVRTGTLAFSVTLFTVFVAFVGI AVLLYRRRPHIGGELGGPRGPKLATTALFLGLWFLYIL 908

Qy 909 FATLEAYCYIKGF 921
 ||:|:|:|:|:|
 Db 909 FASLEAYCHIRGF 921

RESULT 12

NKX1_BOVIN

ID NKX1_BOVIN STANDARD; PRT; 1216 AA.
 AC Q28139; 046384;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
 DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
 GN SLC24A1 OR NCKX1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;
 RP 647-660 AND 1119-1136.
 RC TISSUE=Retina;
 RX MEDLINE=92258377; PubMed=1582405;
 RA Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
 RA Cook N.J.;
 RT "Primary structure and functional expression of the Na/Ca,K-exchanger
 RT from bovine rod photoreceptors."
 RL EMBO J. 11:1689-1695(1992).
 RN [2]
 RP SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).

RC TISSUE=Retina;
 RX MEDLINE=98138491; PubMed=9478004;
 RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
 RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
 RL comparison with a revised bovine sequence.";
 RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
 CC -!- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q28139-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q28139-2; Sequence=VSP_006159;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Retina.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; X66481; CAA47108.1; -.
 DR EMBL; AF025664; AAB88884.1; -.
 DR PIR; S20969; S20969.
 DR InterPro; IPR004817; K_NaCaexchang.
 DR InterPro; IPR004481; K_NaCaexchng.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00927; 2A1904; 1.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Phosphorylation; Signal; Repeat; Alternative splicing.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1216 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 39 446 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 447 467 POTENTIAL.
 FT DOMAIN 468 491 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 492 512 POTENTIAL.
 FT DOMAIN 513 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 519 539 POTENTIAL.
 FT DOMAIN 540 557 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 558 578 POTENTIAL.
 FT DOMAIN 579 579 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 580 600 POTENTIAL.

FT	DOMAIN	601	1024	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1025	1045	POTENTIAL.
FT	DOMAIN	1046	1052	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1053	1073	POTENTIAL.
FT	DOMAIN	1074	1088	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1089	1109	POTENTIAL.
FT	DOMAIN	1110	1127	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1128	1148	POTENTIAL.
FT	DOMAIN	1149	1157	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1158	1178	POTENTIAL.
FT	DOMAIN	1179	1185	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1186	1206	POTENTIAL.
FT	DOMAIN	1207	1216	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	796	928	8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-
FT				I-Q-A-G-E-[GA]-G-E-V-[EK]-G.
FT	REPEAT	796	811	1 (APPROXIMATE).
FT	REPEAT	812	828	2.
FT	REPEAT	829	845	3.
FT	REPEAT	846	862	4.
FT	REPEAT	863	879	5.
FT	REPEAT	880	896	6.
FT	REPEAT	897	913	7.
FT	REPEAT	914	928	8 (APPROXIMATE).
FT	REPEAT	488	528	ALPHA-1.
FT	REPEAT	1096	1127	ALPHA-2.
FT	DOMAIN	984	1009	POLY-GLU.
FT	MOD_RES	652	652	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	303	303	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	868	884	Missing (in isoform 2).
FT				/FTId=VSP_006159.
FT	CONFLICT	84	84	MISSING (IN REF. 1; AA SEQUENCE).
FT	CONFLICT	234	234	MISSING (IN REF. 1; AA SEQUENCE).
FT	CONFLICT	244	245	MISSING (IN REF. 1; AA SEQUENCE).
FT	CONFLICT	857	857	A -> G (IN REF. 2).
SQ	SEQUENCE	1216 AA;	131614 MW;	39F149A74D1D0523 CRC64;

Query Match 6.4%; Score 306.5; DB 1; Length 1216;
 Best Local Similarity 21.4%; Pred. No. 1e-11;
 Matches 202; Conservative 113; Mismatches 324; Indels 305; Gaps 38;

Qy	77	VIVYFVALIYMFLGVSIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: :: :: :: : : :: :	::: : :
Db	449	VVLHIFGMMYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG	490
Qy	136	LTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGET	194
		: : :: : : :	:
Db	491	ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S	541
Qy	195	RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCVL-LA	248
		: : : :: :: : : :	:
Db	542	REILNL-----TWWPLFRDITFYIFDLMLLILFFLDLIAWWESVLLLLLAYAFYVFTMK	595
Qy	249	WVADKRLLFYKYMHHK-----YRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDG	299
		: :: : :: :: :: :	:
Db	596	WNQQLELWVKEQLNKRPAKVMALGDLSPGDGTVVVDEQQDNKKLKLSSMLTRG-----S	651

DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
 GN SLC24A1 OR NCKX1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=Sprague-Dawley; TISSUE=Eye;
 RX MEDLINE=20217335; PubMed=10751314;
 RA Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
 RA Lytton J.;
 RT "Alternatively spliced isoforms of the rat eye
 RT sodium/calcium+potassium exchanger NCKX1.";
 RL Am. J. Physiol. 278:C651-C660(2000).
 RN [2]
 RP SEQUENCE OF 1067-1155 FROM N.A.
 RA White K.E., Gesek F.A., Friedman P.A.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q9QZM6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9QZM6-2; Sequence=VSP_006161;
 CC Name=3;
 CC IsoId=Q9QZM6-3; Sequence=VSP_006162;
 CC Name=4;
 CC IsoId=Q9QZM6-4; Sequence=VSP_006163;
 CC -!- TISSUE SPECIFICITY: Highly expressed in the eye.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; AF176688; AAD53121.1; -.
 DR EMBL; U49235; AAB37753.1; -.
 DR InterPro; IPR004817; K_NaCaexchang.
 DR InterPro; IPR004481; K_NaCaexchnng.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00927; 2A1904; 1.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.

KW	Vision; Transport; Antiport; Symport; Calcium transport;		
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;		
KW	Alternative splicing.		
FT	SIGNAL	1	38
FT	CHAIN	39	1181
FT	DOMAIN	39	419
FT	TRANSMEM	420	440
FT	DOMAIN	441	464
FT	TRANSMEM	465	485
FT	DOMAIN	486	491
FT	TRANSMEM	492	512
FT	DOMAIN	513	519
FT	TRANSMEM	520	544
FT	DOMAIN	545	552
FT	TRANSMEM	553	569
FT	DOMAIN	570	989
FT	TRANSMEM	990	1010
FT	DOMAIN	1011	1017
FT	TRANSMEM	1018	1038
FT	DOMAIN	1039	1053
FT	TRANSMEM	1054	1074
FT	DOMAIN	1075	1092
FT	TRANSMEM	1093	1113
FT	DOMAIN	1114	1121
FT	TRANSMEM	1122	1142
FT	DOMAIN	1143	1150
FT	TRANSMEM	1151	1171
FT	DOMAIN	1172	1181
FT	REPEAT	461	501
FT	REPEAT	1061	1092
FT	DOMAIN	730	905
FT	REPEAT	730	741
FT	REPEAT	742	754
FT	REPEAT	755	766
FT	REPEAT	767	778
FT	REPEAT	779	791
FT	REPEAT	792	804
FT	REPEAT	805	817
FT	REPEAT	818	830
FT	REPEAT	831	843
FT	REPEAT	844	856
FT	REPEAT	857	869
FT	REPEAT	870	881
FT	REPEAT	882	893
FT	REPEAT	894	905
FT	DOMAIN	952	974
FT	MOD_RES	625	625
FT	CARBOHYD	271	271
FT	VARSPLIC	598	710
FT			
FT	VARSPLIC	616	710
FT			
FT	VARSPLIC	652	679
FT			
SQ	SEQUENCE	1181 AA;	129980 MW; B063C1C1193696AE CRC64;

Query Match

6.3%; Score 303.5; DB 1; Length 1181;

Best Local Similarity 20.4%; Pred. No. 1.5e-11;

Matches 194; Conservative 131; Mismatches 305; Indels 321; Gaps 40;

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Qy      77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
      |:::  :|:::  ::|:  |  |::  |||  :      :::  :|  |:
Db      422 VVLHIFGMTYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG 463

Qy      136 LTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGET 194
      |  |  |  |||:  |||  |  ||:  ::|  |||||  ||:  :|  |  :
Db      464 ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 514

Qy      195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCV---- 245
      |:|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
Db      515 REILNL-----TWWPLFRDVSFYILDLSMLIVFFLDLSLIAWWESLLLLLAYALYVFTMK 568

Qy      246 ----LLAWVADK--RLLFYKYMHKKYRTDKHRGIIETEGDHPKGIEM-----DGK 290
      :  |  |  ::  |  |  |  :  |  |  |  |  |  :  :
Db      569 WNKQIERWVKEQLSRPVAKVMA LGDLSKPSDGAIEENEQQDNKKLKLPSVLTRGSSSAS 628

Qy      291 MMNS-----HFLDGNLVPL----EGKEVDESRRMIRILKDLK-----QKHP----- 328
      :  |  |  :  |  :|  ||  |  :  |  |  :  |  |  :  :  |
Db      629 LHNSIIRSTIYHMLHSLDPLGEARPSKDKQESLNQEARVLPQTKAESSSDEEPAELPA 688

Qy      329 -----EKDL DQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGN 367
      ::|::|  :  :  :  :  :  :  |  :  :  |
Db      689 VTVTPAPAPEDKGDQEEDPGCQEDVDEAEHRGDMTGEEGERETEA----EGKKDEEGETE 744

Qy      368 ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSK 427
      :|  ::  :  :  :  |  |  |  :  |  |
Db      745 AERKEDGQEEETETKGKEKQEGETES-----EGKD--- 774

Qy      428 TMYVDYKTEDGSANAGADYE---FTEGTVVLKPGETQKEFSVGIIDDDIFE----- 475
      :  :  |  :  ||:|  ||  |  ||:|  |  |  :  |
Db      775 ----EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEE---GTEDEQEGETEAEGKEVE 827

Qy      476 -----EDEHFFVRLSNVRIEEEQPE---EGMPPAIFNSLPLPRAVLASPCVATVT 522
      |  |  |  |  |  |  |  :  |  |  |  |
Db      828 QEGETEAEGKEVEH-----EVETEAERKETNHEGETEAEGK----- 863

Qy      523 ILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFED 582
      :  |  |  |  :  |  |  :  |  |  |  |  |  :  |  :  :
Db      864 --EADHEGETEAEGNVEHQGE-----TEAEGKV-----EHEGETEAEGKDEHE 904

Qy      583 TYGELEFKNDETVKTIRVKIVD---EEEYERQENFFIALGEPKWMERGISDVTDRKLTME 639
      |:  |  :  |:|  ::  |  |  |  :  |  |  |  |  |  :  :
Db      905 --GQSETQADDT-----EVKDGEGEAEANAEDQCETAQGEKGADGGGSDGGDSEEEED 956

Qy      640 EEEAKRIAEMGKPVLGHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEA 699
      ||:  :  :  |  |  |
Db      957 EEDEEE-----EEEE----- 967

Qy      700 ITVSAAGDEDEDESGEERLPSCFDY-----VMHFLT VFWKVL FACVPPT EYCHGWAC 751
      ::|::|  ||  |  :  :  :  |  |  |  :  :|
Db      968 -----EEEEEESEE--PLSLEWPESRQKQAIYLFLLPIVFPLWLTIPDVRREQARKF 1018

Qy      752 FAV----SILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQ 807
      |  :  ||:  |  |  :  :  |  |  |||:  :  :  :  :|  |||:|  |  |  :
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Db 1019 FVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARK 1078

Qy 808 DVYADASIGNVTGSNAVNVFLGIGLAWSVAAYIYWALQGQEFHVSA-GTLAFSVTLFTIFA 866
 : | :: : ||| :: :: | : :: || | ||: | | | :

Db 1079 GL-GDMAVSSSVGSNIFDITVGLPVPWLLFSLINAL--QPIPVSSNGLFCAIVLLFLMLL 1135

Qy 867 FVCISVLLYRRRPHLGGEGLGGPRGCKLATTW-----LFVSLWLLYILFATL 912
 || | : || | : :: ||| : | :

Db 1136 FVIFSI-----ASCK----WRMNKILGFTMFLLYFVFLVI 1166

RESULT 14

NKX1_HUMAN

ID NKX1_HUMAN STANDARD; PRT; 1099 AA.

AC O60721; O43485; O75184;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 1) (Retinal rod Na-Ca+K exchanger).

GN SLC24A1 OR NCKX1 OR KIAA0702.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Retina;

RX MEDLINE=99072302; PubMed=9856482;

RA Tucker J.E., Winkfein R.J., Murthy S.K., Friedman J.S., Walter M.A.,

RA Demetrick D.J., Schnetkamp P.P.M.;

RT "Chromosomal localization and genomic organization of the human

RT retinal rod Na-Ca+K exchanger.";

RL Hum. Genet. 103:411-414(1998).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Retina;

RX MEDLINE=98138491; PubMed=9478004;

RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;

RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger:

RT comparison with a revised bovine sequence.";

RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).

RN [3]

RP SEQUENCE OF 1-999 FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.";

RL DNA Res. 5:169-176(1998).

CC -!- FUNCTION: Critical component of the visual transduction cascade,

CC controlling the calcium concentration of outer segments during

CC light and darkness. Light causes a rapid lowering of cytosolic

CC free calcium in the outer segment of both retinal rod and cone

CC photoreceptors and the light-induced lowering of calcium is caused

CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O60721-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O60721-2; Sequence=VSP_006160;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Found only in the outer segments of retinal
 CC rod photoreceptors.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; AF062921; AAC16732.1; -.
 DR EMBL; AF062922; AAC77912.1; -.
 DR EMBL; AF026132; AAB97832.1; -.
 DR EMBL; AB014602; BAA31677.1; ALT_SEQ.
 DR Genew; HGNC:10975; SLC24A1.
 DR MIM; 603617; -.
 DR GO; GO:0019867; C:outer membrane; NAS.
 DR GO; GO:0008273; F:calcium, potassium:sodium antiporter activity; NAS.
 DR GO; GO:0006816; P:calcium ion transport; NAS.
 DR GO; GO:0009642; P:response to light intensity; NAS.
 DR GO; GO:0007601; P:vision; NAS.
 DR InterPro; IPR004817; K_NaCaexchang.
 DR InterPro; IPR004481; K_NaCaexchnng.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00927; 2A1904; 1.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1099 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 39 452 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 453 473 POTENTIAL.
 FT DOMAIN 474 497 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 498 518 POTENTIAL.
 FT DOMAIN 519 522 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 523 543 POTENTIAL.
 FT DOMAIN 544 563 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 564 584 POTENTIAL.
 FT DOMAIN 585 585 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 586 606 POTENTIAL.
 FT DOMAIN 607 907 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 908 928 POTENTIAL.

FT	DOMAIN	929	935	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	936	956	POTENTIAL.
FT	DOMAIN	957	971	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	972	992	POTENTIAL.
FT	DOMAIN	993	1010	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1011	1031	POTENTIAL.
FT	DOMAIN	1032	1039	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1040	1060	POTENTIAL.
FT	DOMAIN	1061	1068	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1069	1089	POTENTIAL.
FT	DOMAIN	1090	1099	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	494	534	ALPHA-1.
FT	REPEAT	979	1010	ALPHA-2.
FT	DOMAIN	860	890	POLY-GLU.
FT	MOD_RES	658	658	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	631	648	Missing (in isoform 2).
FT				/FTId=VSP_006160.
FT	CONFLICT	516	516	V -> I (IN REF. 2).
SQ	SEQUENCE	1099 AA;	121374 MW;	3911856BB088B5FD CRC64;

Query Match 6.1%; Score 293; DB 1; Length 1099;
 Best Local Similarity 21.7%; Pred. No. 6.4e-11;
 Matches 191; Conservative 122; Mismatches 268; Indels 298; Gaps 42;

Qy	77	VIVYFVALIYMFLGVSIIDR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: :: : :: :: : ::: :	
Db	455	VVLHVFGMMYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG	496
Qy	136	LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIGICVYVIPDGET	194
		: : :: : : :	
Db	497	ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCSLF-----S	547
Qy	195	RKIKHLRVFFITAAWSIFAYIWLY----MILAVFSPGVVQVWEGLLTLFFFPVCVLLAW	249
		: : : : :: :: : :	
Db	548	REILNL-----TWWPLFRDVSFYILDLMILFFLDSLIAWWESLL-----LLLAY	593
Qy	250	VADKRLLFYKYMHHKKYRTDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEV	309
		: : : :: :	
Db	594	A-----FYVFTMK---WNKHIEVWVKEQ-----	613
Qy	310	DESRREMIRI--LKDLKQKHPEKDLQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGN	367
		: :: : : : :: ::: ::	
Db	614	-LSRRPVAKVMALEDL-----SKPGDGAI-----AVDELQDNK---KLKLPSLLT----	654
Qy	368	ILKKHAAEQAKKASSMSEVHTDEPEDFISKVF---FDPCSYQCLENCGAVLLTVVRKGGD	424
		: : : : :	
Db	655	-----RGSSSTSLHNSTIRSTIYQLMLHSLDP-----LREVR----	686
Qy	425	MSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRL	484
		:: : : : :	
Db	687	LAK-----EKEEESLNQGARAQ-PQAKAESKP-----	712
Qy	485	SNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDD--DHAGIFTFECDTIHVS	542
		: : : : :: : : :	
Db	713	-----EEEEPAK-LPAVTVTPAPVP-----DIKGDQKENPG---GQEDVAEA	750

Qy 543 ESIGVMEVKVLRTSG-----ARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND---E 593
 || || : | : | | | | : | | : | | | | |
 Db 751 ESTGEMPGEETAGEGETEEKSGGETQPEGEGETETQKGEECEDE-NEAEGKGDNEGE 809

Qy 594 TVKTIRVKIVD----EEEYERQENFFIALGEPKWMERGISD--VTDRKLTMEEEEAKRIA 647
 | : : | | | | | | | | : | : | : | : | :
 Db 810 DEGEIHAEDGEMKNGEGETESQELSAENHGEAKNDEKGVEDGGSGDGGDSEEEEEEEEEEQ 869

Qy 648 EMGKPVLGHEHPKLEVIIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGD 707
 | : | | | :
 Db 870 E-----EEEEEEQEEEEEE-----E 885

Qy 708 EDEDESGEERLPSCFDY-----VMHFLTTFWKVLFACVPPTEYCHGWACFAV----S 755
 | : | | | | : : | | : | | | | |
 Db - 886 EEEEEKGNEE-PLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRREQSRKFFVFTFLGS 944

Qy 756 ILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
 | : | | : : | | | : : : : : | | : | : : | : :
 Db 945 IMWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGL-GDMAV 1003

Qy 816 GNVGTGSNAVNVFLGIGLAWSVAAYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLY 875
 : | | : : : : : : | | | | : | : | : | :
 Db 1004 SSSVGSNIFDITVGLPVPWLLFSLINGLQPVVPS-SNGLFCAIVLLFLMLLFVISSI--- 1059

Qy 876 RRRPHLGELGGPRGCKLATTW-----LFVSLWLLYILF 909
 | | | : : | : | : | :
 Db 1060 -----ASCK----WRMNKILGFTMFLLYFVF 1081

RESULT 15

NKX3_MOUSE

ID NKX3_MOUSE STANDARD; PRT; 645 AA.
 AC Q99PD7; Q99JR2; Q99PD8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sodium/potassium/calcium exchanger 3 precursor (Na(+)/K(+)/Ca(2+)-
 DE exchange protein 3).
 GN SLC24A3 OR NCKX3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and CD-1; TISSUE=Brain, and Embryonic stem cells;
 RX MEDLINE=21303617; PubMed=11294880;
 RA Kraev A., Quednau B.D., Leach S., Li X.-F., Dong H., Winkfein R.,
 RA Perizzolo M., Cai X., Yang R., Philipson K.D., Lytton J.;
 RT "Molecular cloning of a third member of the potassium-dependent
 RT sodium-calcium exchanger gene family, NCKX3."
 RL J. Biol. Chem. 276:23161-23172(2001).
 RN [2]
 RP SEQUENCE OF 323-645 FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Transports one Ca(2+) and one K(+) in exchange for four
 CC Na(+) (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Abundant in the brain. Highest levels found in
 CC selected thalamic nuclei, hippocampal CA1neurons and in layer IV
 CC of the cerebral cortex.

CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.

CC -----
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 CC -----

DR EMBL; AF314821; AAG60049.1; -.

DR EMBL; AF314822; AAG60050.1; -.

DR EMBL; BC005742; AAH05742.1; -.

DR MGD; MGI:2137513; Slc24a3.

DR GO; GO:0008273; F:calcium, potassium:sodium antiporter activity; IDA.

DR InterPro; IPR004481; K_NaCaexchn.

DR InterPro; IPR004837; NaCa_Exmemb.

DR Pfam; PF01699; Na_Ca_Ex; 2.

DR TIGRFAMs; TIGR00367; TIGR00367; 1.

KW Transport; Antiport; Symport; Calcium transport; Potassium transport;

KW Sodium transport; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 43 POTENTIAL.

FT CHAIN 44 645 SODIUM/POTASSIUM/CALCIUM EXCHANGER 3.

FT DOMAIN 44 106 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 107 127 POTENTIAL.

FT DOMAIN 128 151 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 152 172 POTENTIAL.

FT DOMAIN 173 181 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 182 202 POTENTIAL.

FT DOMAIN 203 209 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 210 230 POTENTIAL.

FT DOMAIN 231 234 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	235	255	POTENTIAL.
FT	DOMAIN	256	486	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	487	507	POTENTIAL.
FT	DOMAIN	508	512	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	513	533	POTENTIAL.
FT	DOMAIN	534	551	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	552	572	POTENTIAL.
FT	DOMAIN	573	582	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	583	603	POTENTIAL.
FT	DOMAIN	604	617	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	618	638	POTENTIAL.
FT	DOMAIN	639	645	EXTRACELLULAR (POTENTIAL).
FT	REPEAT	148	188	ALPHA-1.
FT	REPEAT	520	551	ALPHA-2.
FT	DOMAIN	424	430	POLY-GLU.
FT	CARBOHYD	70	70	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	85	85	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	645 AA;	71914 MW;	C62DEB6CB4A01C96 CRC64;

Query Match 5.5%; Score 266; DB 1; Length 645;
 Best Local Similarity 19.1%; Pred. No. 1.7e-09;
 Matches 162; Conservative 94; Mismatches 216; Indels 374; Gaps 30;

Qy	77	VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: : : :: : : : : : :	
Db	109	VVLHVLCA MYFYALAIVCDDFFVPSLEKICERLH-----LSEDVAG	150
Qy	136	LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET	194
		: : : : : :	
Db	151	ATFMAAGSSAPELFTSVIGV----FITKGDVGVTIVGS AVFNILCIIGVCGLFA--GQV	204
Qy	195	RKIKHLRVFFITA A W-----SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAW	249
		: : : : : : : : : : : : :	
Db	205	VAL-----SSWCLLRDSIYYTSLVVALIVFIYDEKVSWWESLVLVLMYLIYIVI--	253
Qy	250	VADKRLLFYKYM HKKYRTDKHRGII IETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEV	309
		: : : :	
Db	254	-----MKYNACI HQCFERRTKG-----AGNMVNG--LANN-----AEI	284
Qy	310	DESRRMIRILKDLKQKHPEKDLDQLVEMANY YALSHQQKSR AFYRIQATRM MTGAGN IL	369
		:	
Db	285	DDS-----	287
Qy	370	KKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTM	429
		:	
Db	288	-----SNCDATV-----	294
Qy	430	YVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVGIIDDDIFEED EHFVRLSNVRI	489
		: : : : :	
Db	295	-----VLLKKANFHRKASVIMVDE-----LLSAYPH	320
Qy	490	EEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVME	549
		: : : : : : : : :	
Db	321	QLSFSEAGLRIMITSHFP-PKTRLS----MASRMLINERQRLINSRAYTNGESEVAIKIP	375
Qy	550	VKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYE	609
		: : : : : :	

Db 376 IKHTVENGT-GPSSAPDRGVNGTRR-----DDIVAETD-----NETENE 413
 Qy 610 RQENFFIALGEPKWMERGISDVTDRKLTMEEEEEAKRIAEMGKPVLGHEHPKLEVIIIEESYE 669
 : : | | | |
 Db 414 NEDN-----ENNESD-----EEEE----- 428
 Qy 670 FKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDE-----SGE-ERLP 719
 : : | | : : | :
 Db 429 -----DEDDDEGPYTPFDPPSGKLETVK 451
 Qy 720 SCFDYVMHFLTTFVFWKVLFAVPPTEYCHGW-----ACFAVSILIIIGMLTAIIGDLASHFG 774
 : : : | : : | | : : | : : : : :
 Db 452 WFTWPLSF-----VLYFTVPNCNKPH-WEKWFMTFASSTLWIAAFSYMMVWMVTIIG 504
 Qy 775 CTIGLKDSVTAVVFVAFGTSVPDTEFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
 : : : : : : | | | | : : : : : :
 Db 505 YTLGIPDVIMGITFLAAGTSVPDCMASLIVARQGM-GDMAVSNSIGSNVFDILIGLGLPW 563
 Qy 835 SVAAI-----YWALQGQEFHVSAGTLAFSV-----TLFTIFAF 867
 : : : | : | | | : : | :
 Db 564 ALQTLAVDYGSIYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKNWQLDKKLGCGCLFLYGVF 623
 Qy 868 VCISVL 873
 : | : :
 Db 624 LCFSIM 629

Search completed: June 24, 2004, 16:12:39
 Job time : 22.3323 secs